Access DB# 8/357

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Art Unit: Phone Nu		Examiner # :	Date:
Mail Box and Bldg/Room Leasting	umber 30	Serial Number:	
Mail Box and Bldg/Room Location:		Results Format Preferred (c	ircle): PAPER DISK E-MA
If more than one search is submit	ted, please pric	oritize searches in order o	of need.
Please provide a detailed statement of the se Include the elected species or structures, key utility of the invention. Define any terms the known. Please attach a copy of the cover she	earch topic, and desc ywords, synonyms, a lat may have a speci	cribe as specifically as possible the acronyms, and registry numbers, all meaning. Give examples or re-	subject matter to be searched
Title of Invention:			
Inventors (please provide full names):			
Earliest Priority Filing Date:			
For Sequence Searches Only Please include appropriate serial number.			ued patent numbers) along with the
appropriace serial number.			
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. () Ø	ype of Search		where applicable
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ate Completed: 12/2/02 Li	tigation	Lexis/Nexis	
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PTO-1590 (8-01)

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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      GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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XC7123

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ALIGNMENTS

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coagulation factor

RESULT 2 A55315

cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

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R;Mukasa, T.; Urase, K.; Momoi, M.Y.; Kimura, I.; Momoi, T. Biochem. Biophys. Res. Commun. 231, 770-774, 1997
A;Title: Specific expression of CPP32 in sensory neurons of A;Reference number: JC5410; MUID:97224429; PMID:9070890
A;Accession: JC5410
A;Status: nucleic acid sequence not shown
                           A; Molecule type: mRNA
A; Residues: 1-277 <MUK>
A; Cross-references: DDBJ:D86352
                                                                                                                                                                                                                            CPP32 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change
C;Accession: JC5410
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JC5410
A; Experimental source:
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A;Molecule type: mRNA
A;Residues: 1-189,'E',191-277 <RES>
A;Cross-references: EMBL:U26943; NID:g857568; PIDN:AAA74929.1; PID:g857569
C;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Yama/CPP32 beta, a mammalian homolog of CED-3, A;Reference number: A56924; MUID:95292347; PMID:7774019 A;Accession: I39005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Tewari, M.; Quan, L.1
Cell 81, 801-809, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.Alternate names: cysteine proteinase CPP32
c;Species: Homo sapiens (man)
c;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
c;Accession: A55315; S58899; I39005
R;Fernandes-Alnemri, T; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A;Title: CPP32, a novel human apoptotic protein with homology to Caenorhabd:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 29-46; 176-189, 'E', 191-193 < NIC>
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-277 <FER>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a novel human apoptotic protein with homology ber: A55315; MUID:95074098; PMID:7983002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L.T.; O'Rourke,
      embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.5%; Score 718; DB 2; 50.5%; Pred. No. 1.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
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167437
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A; Residues: 1-212 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                            nulosa cells of the ovarian follicle.
A;Reference number: I53300; MUID:96042508; PMID:7588240
A;Accession: I67437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Endocrinology 136, 5042-5053, 1995
                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U34685; NID:g1004370; PIDN:AAC52261.1; PID:g1004371
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                                                                                                                                           83
                                                                                                                                                                                                                                 60 YNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKM 119 | | | : | : | | | | : : : : |
                                                                                                                                                                                                                                                                                                   Local
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                                                                                      LFFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGS
 WFIQSLCAMLKLYAHKLEFMHILTRVN
                                                                                                                                       MELMDSVSKEDHSKRSSFVCVILSHGDEGVIFGTNGPVDLKKLTSFFRGDYCRSLTGKPK
                                                                                                                                                                          QDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPK 179
                                                                                                                                                                                                             YKMDYPEMGLCIIINNKNFHKSTGMSARNGTDVDAANLRETFMALKYEVRNKNDLTREEI
                                  WFVQALCSILEEHGKELEIMQILTRVN
                                                                     LFIQACRGTELDSGIETDSGADDDVACQ ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFYCVILSHGDEGVIFGTNGPVDLKKLTSFFRGDYCRSLTGKPKLFIIQACRGTELDCGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKTSVDSKSINNFGVKTIHGSKSVDSGIYLDS-----SYKMDYPEMGICIIITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEDSVDAKPDRSSFVPSLFSKKK--KNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144;
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                                                                                                                                                                                                                                                                                                                                                      cysteine proteinase;
                                                                                                                                                                                                                                                                                                   Similarity
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52.7%;
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                                                                                                                                                                                                                                                                                 37;
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                                                                                                                                                                                                                                                                                                                                                      hydrolase
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                                                                                                                                                                                                                                                                                                                  Score 580.5;
                                                                                                                                                                                                                                                                                  Mismatches
211
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                                                                                                                                                                                                                                                                                                   No. 9.8e-43;
                                                                     KKPVEADFLYAYSSAPGYYSWRNSRGGS
                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                  58;
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                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                   Length
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interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhal Species: Caenorhabditis elegans C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_chang C:Accession: A49429; T37312 C:R:Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.

RESULT A49429

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Caspase-9 long chain - mouse
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: JC7123
R:Fujita, E: Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A:Title: Akt phosphorylation site found in human caspase-9 is absent in mous A:Reference number: JC7123; MUID:20001956; pMID:10529400
A:Accession: JC7123
A:Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-503 <YU
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A;Gene: ced-3
A;Introns: 45/3;
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A; Residues: 1-417,'R',419-503 <YU2>
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A;Reference number: A49429; MUID:94061982; PMID:8242740
A;Accession: A49429
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                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-454 <FUJ>
A;Cross-references: DDBJ:AB019600; NID:g6440941; PID:g6440942
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;Cross-references: GB:L29052; NID:g6503232; PIDN:AAA27982.2; PID:g6503233
;Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBIP:139826)
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                                                                191 YTLDSDPCGHCLIINNVNFCRSSGLGTRTGSNIDRDKLEHRFRWLRFMVEVKNDLTAKKM 250
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QDLLKKASEEDHTNAACFACILLSHGEE-----NVIYGKDGVT-PIKDLTAHFRGDRC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WRKKPSQADILIAYATTAQYVSWRNSARGSWFIQAVCEVFSTHAKDMDVVELLTEVNKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIVFVQACRGERRDNGF-----PVLDSVDGVPAFLRRGWDNRDGPLFNFLGCVRPQVQQV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLFFIQACRGTELDDAIQADSGPINDT-DANPRY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDFAKHESHGDSAIL--VILSHGEENVIIGVDDIPISTHEIYDLLNAANAPR---LANKP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EK-LGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKN-VTMRSIKTTRDRVPTYQYNMNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGFQTSQGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSPRGMCLIINNEHFEQ---MPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94/2; 179/1; 289/3; 361/1; 403/3; 483/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -NILKOMPEMTSRLLKKFYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.4%;
                                                                                                                                                                      23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Mismatches 117;
                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 377; DB 2; Pred. No. 1.1e-24;
                                                                                                                                                  Score 371.5; DB
Pred. No. 3e-24;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494
                                                                                                                                                                                            DB 2;
                                                                                                                                                    96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                            Length
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                     absent in mouse
                                                                                                                                                  45;
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                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465
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                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                  caspase-9
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C:Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-
C;Accession: G02635
R;Duan, H; Orth, K; Chinnaiyan, A.M.; Po
submitted to the EMBL Data Library, April
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G02635
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                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-416 < DUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: H01513
A; Accession: G02635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                          213 VLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDGCPVSVEKIVNIFNGTSC
                                                                                                                                                                                                                                                                                                                  60 YMMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKM 119
                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                 YILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTLLEKPKLFFIQACRGTELDD----AIQADSGPINDTDANPR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTALMEMAHRNHRALDCFYVYILSHGCQASHLQFPGAYYGTDGCSYSIEKIYNIFNGSGC
                                                                                   --IPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVA 270
                                                                                                                                                                                                                                           QDLLKKASEEDHTNAACFACILLSHGEE-----NVIYGKDGV-TPIKDLTAHFRGDRC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHFESQSDDPHFHEK----KQIPCVVSMLTKELYF 301
                             RHFESQSDDPHFHEK - - - KQIPCVVSMLTKELYF
                                                                 SSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVS
                                                                                                                                        PSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQLDAI
                                                                                                                                                                           KTLLEKPKLFFIQACRGTELDDAIQADS------GPINDTDANPRYK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSLPTPSDILVSYSTFPGFVSWRDKKSGSWYIETLDGILFQWARSEDLQSLLLRVANAVS 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSLGGKPKLFFIQACGGEQKDHGFEVACTSSQGRTLDSDSEPDATPFQEGPRPLDQLDAV
                                                                                                                                                                                                                                                                                                                                                    88;
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
·VKGIYKQMPGCFNFLRKKLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -EKGTYKQIPGCFNFLRKKLFF
                                                                                                                                                                                                                                                                                                                                                                   22.0%;
                                                                                                                                                                                                                                                                                                                                                    41; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                 Score 354.5; DB 2
Pred. No. 7.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poirier, G.G.;
il 1996
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                              301
413
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R;Burton, J. submitted to the EMBL Data Library, October 1996 a.Reference number: Z19214 hypothetical protein C48D1.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T20038 C;Genetics: A;Gene: CESP:C48D1.2 A; Molecule type: DNA A; Residues: 1-495 <WIL> A; Reference number: A; Accession: T20038 A; Experimental source: A; Status: preliminary; translated from GB/EMBL/DDB. T20038 A; Cross-references: position: EMBL: Z81049; clone C48D1 PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2 15-Oct-1999

A;Map

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A;Reference number: A54821; MUID:94373811; PMID:8087842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apoptosis regulator ICH-1, stimulatory form L - human C;Species: Romo sapiens (man) C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999 C;Accession: A54821 R; Wang, L; Miura, M; Bergeron, L; Zhu, H; Yuan, J. Cell 78, 739-750, 1994 R;Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative.
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A; Residues: 1-435 <WAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
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 413
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                                                                                                                                                                                                                                                                                  60 YNMNFEKLGKCIIINNKNFDKYTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKM 119
                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
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                                                                                                                                                                                                                                                    YRLQSRPRGLALVLSNVHFTGEKELEFRSGGDVDHSTLVTLFKLLGYDVHVLCDQTAQEM 234
                                                                                                                                                                                                                      QDLLKKASEEDHTNAACFACI--LLSHGEENVIYGKDG-VTPIKDLTAHFRGDRCKTLLE 176
 KEMSEYCSTLCRHLY
                                                           LKGTAAMRNTKRGSWYIEALAQVFSERACDMHVADMLVKVN-ALIKDREGYAPGTEFHRC
                                                                                         VPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEK 285
                                                                                                                                                                                       QEKLQNFAQLP-AHRVTDSCIVALLSHGVEGAIYGVDGKLLQLQEVFQLFDNANCPSLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVELLTEVNKKVA 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAPR - - - LANKPKIVFVQACRGERRDNGF - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVFDEKTMYRNESSPRGMCLIINNEHFEQ---MPTRNGTKADKDNLTNLFRCMGYTVICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNAFPSQPSSANSSFT----GCSSLGYSSSRNRSFSKASGPTQYIFHEEDMNFVDAPTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRV----PT----YQYNMNF---
                             KQIPCVVSMLTKELY
                                                                                                                         KPKMFFIQACRGDETDRGVDQQDGKNHAGSPGCEESDAGKEKLPKMRLPTRSDMICGYAC
                                                                                                                                                       KPKLFFIQACRGTELDDAIQADSGP-----INDTDAN----PRYKIPVEADFLFAYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLGCVRPQVQQVWRKKPSQADILIAYATTAQYVSWRNSARGSWFIQAVCEVFSTHAKDMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGDRCKTLLEKPKLFFIQACRGTELDDAIQADSGPINDT-DANPRY--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDCSCAKMQDLLKK-ASEEDHTNAACFACILLSHGEENVIYGKDGVT----PIKDLTAHF
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                                                                                                                                                                                                                                                                                                                       75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELE
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                                                                                                                                                                                                                                                                                                                                                                                   splicing;
                             300
                                                                                                                                                                                                                                                                                                                                      19.7%;
427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.7%; Score 349.5; DB 2;
31.0%; Pred. No. 2.7e-22;
40. Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 '288/3; 360/1; 402/3; 466/1
                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                   Score 317; DB 2;
Pred. No. 1.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                   apoptosis
                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                PID:g537292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVLDSVDGVPAFLRRGWDNRDGPLFN
                                                                                                                                                                                                                                                                                                                     112;
                                                                                                                                                                                                                                                                                                                                                  Length 435;
                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                     16;
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                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               negative regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                       353
                                                                                                                                                                                       293
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Qy

57

TYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSC | :| | :| | :| | :| | :| | :| | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::

Matches Query Match Best Local

Similarity

18.9%;

Score 305; DB 2; Pred. No. 3.6e-18; 3; Mismatches 96;

Length 826

Indels

36;

Gaps

8

proteinase; hydrolase

Conservative

53;

```
Gene 202, 127-132, 1997
A.Title: Cloning and expression of the cDNA encoding rat A;Reference number: JC6507; MUID:98087427; PMID:9427555
A;Accession: JC6507
A;Gene: csp-2
A;Map position: 4
C;Keywords: cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
T43638
                                                                                      A; Molecule type: mRNA
A; Residues: 564-826 <
                                                                                                                                            A; Cross-references: A; Accession: T43639
                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-826 <SHA>
                                                                                                                                                                                                                                                  J. Biol. Chem. 273, 35109-35117, 1998
A; Title: Identification of multiple Caenorhabditis elegans
A; Reference number: Z22587; MUID:99074291; PMID:9857046
                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision
C;Accession: T43638; T43639
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                                                                      A; Cross-references:
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                                                                                                                                                                                                                                   A; Accession: T43638
                                                                                                                                                                                                                                                                                                         R;Shaham,
                                                                                                                                                                                                                                                                                                                                                                              N; Contains: caspase 2B
                                                                                                                                                                                                                                                                                                                                                                                              caspase-related proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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C;Date: 16-Jul-1999 #sequence_revision 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
JC6507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:U77933; NID:g2769705; PIDN:AAB96379.1; PID:g2769706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-452 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Sato, N.; Milligan, C.E.; Uchiyama,
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                                                                                                                           Status: preliminary; translated
                                                       Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYACLKGNAAMRNTKRGSWYIEALTQVFSERACDMHVADMLVKVN-ALIKEREGYAPGTE 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQ--YNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS
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                                                                        EMBL: AF088289;
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29.3%;
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Pred. No. 1.7e-18;
                                                                                                                             from
                                                                      NID:g4063375;
                                                                                                                                                             NID:g4063373; PIDN:AAC98295.1;
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                                                                        PIDN: AAC98296.1;
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                                                                      PID:g4063376
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A; Residues: 269-536 <
A; Cross-references: E
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A;Title: Identification of multiple Caenorhabditis elegans caspases
A;Reference number: Z22587; MUID:99074291; PMID:9857046
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RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description: probably acts in proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
Residues: 1-536 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                      SMLEAIKEFAEMAHTDS--IILFLLSHGDGAGSVFGIDDMPVNVMEVSTYLAYH-----Q 392
                                                                                                                                                                                                                                                                                        KMODLLKKASEEDHTNAACFACILLSHGE-ENVIYGKD----GVTPIKDLTAHFRGDRCK 172
                                                                                                                                                                                                                                                                                                                                                    YQYNMNFEKLGKCIIINNKNFDKYTGMGYRNGTDKDAEALFKCFRSLGFDYIYYNDCSCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SLAKKPKWLMCVCCRGDRIDRAVRCDGFIDNFFDRFPKFFQFMKSKFPSHQTSSSQA
                                                   NVVL---
                                                                                  DPHFHEKKQIPCVVSMLTKELYFSQ 303
                                                                                                                  VIISFSTTDGFTSYRDEEAGTWYIKSMCKVFNKHSKTMHLLDILTETGRNVVTKYENVQG 512
                                                                                                                                                  FLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSD
                                                                                                                                                                                    NLLLKPKWVAVSACRGGKLNMGVPVDGLPALEDKCAPISKFWNLMMSRIMPGTFTSLNAD
                                                                                                                                                                                                                                                                                                                          YCYEMNSNPRGTVLILSNENF---KNMERRVGTKQDEVNLTKLFQKLQYTVICKRNLEAE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDPHFHEKKQIPCVVSMLTKELYF 301
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                                                   KQAPEILSRLTKQWHFSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <SH2>
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Pred. No. 1.4e-16;
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A;Reference number: Z20299
A;Accession: T27021
                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Y48E1B.13 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct.1999 C;Accession: T27021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T2702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Accession: JC/517
R;Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.
                                                                                                                                                      A; Map position:
A; Introns: 79/3
                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z93393; PIDN:CAB07698.1; A;Experimental source: clone Y48E1B
                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-642 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                              R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 19p13.1
A; Introns: 9/3; 59/3; 135/1; 174/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E. Biochem. Biophys. Res. Commun. 277, 655-659, 2000 A;Title: Caspase-14: Analysis of gene structure and mRNA A;Reference number: JC7517; MUID:20517231; PMID:11062009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caspase-14/a - human
                                                                                                                                                                                             A; Gene: CESP:Y48E1B.13
                                                                                                                                                                                                                                                                                                             A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: casp-14/a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AF097874
C;Comment: This enzyme accumulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-242 <ECK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Contents: Epidermal keratinocytes
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-- rocal Similarity
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                 Genetics:
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  361
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YCYEMNSNPRGTVLILSNENF---KNMERRVGTKQDEVNLTKLFQKLQYTVICKRNLEAE 417
                                    YOYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRKRLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQKGSCFIQTLVDVFTK---RKGHILELLTEVTRRMAEAELVQEG-----KARKTNPEIQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSM 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAKPKYYIIQACRGEQRDPGETVGGDEIVMVIKDSPQTIPTYTDALHVYSTVEGYIAYRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEKPKLFFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FQEELEKFQQAIDSREDPVSCAFVVLMAHGREGFLKGEDGEMVKLENLFEALNNKNCQAL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYDMSGARLALILCVTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MQDLLKK----ASEEDHTNAACFACILLSHGEENVIYGKDG-VTPIKDLTAHFRGDRCKTL
                                                                                                                                                        79/3;
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                                                                                                                                                      122/3; 239/2; 286/3; 333/1;
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                                                                             Conservative
                                                                                                                                                                                                                                                                                                               translated from GB/EMBL/DDBJ
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28.0%;
                                                                                             15.5%;
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                                                                             41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                           Score 250; DB 2;
Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 255; DB 2;
Pred. No. 1.6e-14;
6; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       during keratinocyte differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208/3
                                                                                                                                                      417/3;
                                                                                                                                                                                                                                                        GSPDB:GN00020;
                                                                                                                                                        487/1; 589/1;
                                                                                                             Length 642
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A;Description: Sequencing the distal X chromosome of Drosophila melanogaster. A;Reference number: Z17665
A;Accession: T1385
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-488 <CAT>
A;Residues: 1-488 <CAT>
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T13385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: FlyBase:FBgn0020381
A;Map position: X
A;Introns: 30/3; 272/3; 393/3; 445/2
A;Note: EG:115C2.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 115C2.9 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:AL031581; NID:e1320978; PID:e1331441; PIDN:CAA20893.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics
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                                                                               467
                                                                                                                                                                                                                                                            164 AHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAY 223
                                                                                                                                                                                                                                                                                                                            108 VIVYNDCSCAKMODLLKKASEEDHTNAACFACILLSHGEENVIYGKDG-----VTPIKDLT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 STVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFH 283
                                                                                                                                                                                                                                   363
                                                                                                                                                                                                                                                                                                  304 VEAYDNVDHMGIIERIRSACDRSLVRDS-LVVFILSHGFEEAVYASNSIAMKITDIEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             522
                                                                                                              284 EKKQIPCVVSMLTKELYF 301
                                                                                                                                                                                                                                                                                                                                                                                                               53 DRVPTYQYNMNFEKLGKCIIINNKNFDKVTGMGV-----RNGTDKDAEALFKCFRSLGFD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 25.5 hes 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GCIEEQGVEDSAN--EDSVDA---KPDRSSFVPSLFSKKKKNVTMRS-----IKTTR 52
                                                                                                                                                                                                                         CSY----DTLYYKPKLLIIQACQEKLVHKKKPNELFRIDVTTVSPDQHI----DMLRAM
                                                                           DESMVPNVKSTFROHVYF
                                                                                                                                              STVNGYAALRHTQTGSWFTGSLCDAIDRRSASEHIADILTIVTNEVSKKRGS-----N 466
                                                                                                                                                                                                                                                                                                                                                                               -----ENAGIALIINQQKFHRNKFLSPDPLRRRDGTDVDKERLIEVFSSMGYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFES 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TILLEKPKLFFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSW 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KMQDLLKKASEEDHTNAACFACILLSHGE-ENVIYGKD----GVTPIKDLTAHFRGDRCK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.3%; Score 246.5; DB 2; 25.5%; Pred. No. 2.1e-13; tive 58; Mismatches 128;
                                                                           484
                 2002, 12:57:07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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    on ::
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            Score
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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1613
1 MADDQGCIEEQGVEDSANED......EKKQIPCVVSMLTKELYFSQ 303
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  ICE1_DROME
ICE6_MOUSE
ICE6_HUMAN
ICE8_HUMAN
ICEA_HUMAN
CED3_CAEPU
CED3_CAEPU
ICE9_HUMAN
ICE2_CHICK
        ICE2_RAT
I1BC_PIG
I1BC_HORSE
                                 ICEE_HUMAN
ICEE_MOUSE
ICEB_XENLA
ICEA_XENLA
ILBC_FELCA
ICED_BOVIN
ILBC_CANFA
ICE5_HUMAN
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ICE2_MOUSE
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                                                                                                                                                                                              CE_DROME
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Q9mzv6
Q75601
Q9mzv7
P51878
P55215
Q9n2i1
Q9tv13
P43527
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Q92851
Q92856
P45436
P42573
P55211
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002002
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P70677
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                                                                  P55865
                                                                                                                                                                                                                                                                                     Description
                                                                        5 homo sapien
4 mus musculu
4 homo sapien
4 mus musculu
7 xenopus lae
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caenorhabdi
                                                                                                                                                                                    drosophila drosophila
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h caspase-8
       sus scrofa
equus cabal
                        homo sapien
rattus norv
                                        bos taurus
canis famil
                                                        xenopus lae
felis silve
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gallus gall
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CARA_THETN	FA9_MOUSE	RAD1_YEAST	YB55_METJA	FA9_RAT	CFLA_MOUSE	CFLA_HUMAN	ICEC_MOUSE	ICE4_HUMAN	I1BC_MOUSE	ICEB_MOUSE	I1BC_HUMAN	
Q8rbk1	P16294	P06777	Q58555	P16296	035732	015519	008736	P49662	P29452	P70343	P29466	
			methanococc	rattus norv	m casp8 and	h casp8 and	mus musculu				homo sapien	

ALIGNMENTS

RP R	R R R R R R R R R R R R R R R R R R R	RET TERM REPORTED TO SERVICE OF S	RESUICET, ICET, ACC DT DT DT DE DE GN
SEQUENCE FROM N.A. (ALPHA AND ALPHA' ISOFORMS). TISSUE-Fetal lung, and Fetal spleen; MEDLINE-97224489; PubMed-9070923; Juan T.SC., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J., Copeland N.G., Fletcher F.A.; "Identification and mapping of Casp7, a cysteine protease resembling CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."; Genomics 40:86-93(1997). [5] [5] SEQUENCE FROM N.A. (ALPHA ISOFORM). TISSUE-Skin; Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.	Pleen; 96147144; PubMed=8567622; A., Gu Y., Sarnecki C., Caro ication and characterization protease similar to CPP32.", Chem. 271:1825-1828(1996). FROM.N.A. (ALPHA AND BETA IS 96105019; PubMed=8521391; 96105019; PubMed=8521391; s-Alnemri T., Takahashi A., A C., Tomaselli K.J., Wang L., W.C., Litwack G., Alnemri E. novel human apoptotic cystei es. 55:6045-6052(1995).	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606; [1] SEQUENCE FROM N.A. (ALPHA ISOFORM). MEDLINE=96139498; PubMed=8576161; Duan H., Chinnalyan A.M., Hudson P.L., Wing J.P., He WW., Dixit V.M.; "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans cell death protein Ced-3 is activated during Fas- and tumor necrosis factor-induced apoptosis."; J. Biol. Chem. 271:1621-1625(1996).	LT 1 _TCE7_HUMAN STAN P55210; Q13364; Q96 01-OCT-1996 (Rel. 3 01-OCT-1996 (Rel. 3 15-JUN-2002 (Rel. 4 Caspase-7 precursor (ICE-LAP3) (Apoptot CASP7 OR MCH3.

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RT "IN VILLOW CHARMENT E.S.;

RT apoptotic cysteine protease containing two FADD-like domains.";

RI APOPTOTIC CYSTEINE PROTEASE, 93:7464-7469(1996).

CC .i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES

CC RESULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY

CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY

CC REGULATORY ELEMENT BINDING PROFES (PARP) AT A 216-ASP-|-GLY-217

CC REGULATION: CHAPLESSION PROMOTES PROGRAMMED CELL DEATH.

CC -!- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.

CC -!- SUBGUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.

CC -!- SUBGUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.

CC -!- SUBGUNITICALLY ACTIVE.

CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,

CC -ITSUSCE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,

CC -ITSUSCE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,

CC LIVER, KIUNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO

CC SUBGUNITS. PROPERIOE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY

CC SUBGUNITS. PROPERIOE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY

CC CASPASE-7 AND THE LARGE SUBUNIT OF CP932 PROTEASE ALSO OCCUR AND
                                                                                                                                                            PRINTS; PRO0376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
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InterPro: IPR001309; ICE_p20
Pfam: PF00655; ICE_p10; 1.
Pfam: PF00656; ICE_p20; 1.
                                             VARSPLIC
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CAUTION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF.4
BUT AS BETA IS ALREADY DEFINED IN REF.3 WE HAVE CALLED
                                                                                                                                                                                                                                                                                                                                                                                                   VICE VERSA.
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Illrich F., Fritz L.C., Trap
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ELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYY
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Matches 301
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CONFLICT
SEQUENCE
                                                                                                                       "Purification and cDNA cloning of a second apoptosis-related cysteine protease that cleaves and activates sterol regulatory element binding proteins.";
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15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-7 precursor (EC 3.4.22-7) (ICE-Like apoptotic protease
(ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity
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STRAIN-Syrian; TISSUE-Liver;
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                                                                                                                                                                                                                                                                                    CASP7 OR MCH3.
                                                                                                                                                            Pai J.-T., Brown M.S., Goldstein
                                                                                                                                                                         MEDLINE=96224303; PubMed=8643593;
                                                                                                                                                                                                                        NCBI_TaxID=10036;
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HFESQSSDDPHFHEKKQIPCVVSMLTKELYFSQ -> MESCS
VTQAGVQRRDLGRLQPPPPRLAEGPSLMMASPPTRGPSMTQ
MLILDTRSQWKLTSSSPIPRFQAITRGGAQEEAPGLCKPSA
PSWRSTEKTWKSCRSSPG (IN ISOFORM BETA).
C->A: NO APOPTOTIC ACTIVITY.
                                                          93:5437-5442(1996).
ACTIVATION CASCADE OF CASPASES
EXECUTION. CLEAVES AND ACTIVATES STEROL
G PROTEINS (SREBPS). PROTEOLYTICALLY
POLYMERASE (PARP) AT A 216-ASP-1-GLY-217
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Pfam; PF00656; ICE_p20; 1.
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InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
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HSSP; P42574;
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
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                                                                                                                         FSO
                                                                                                                                                            FVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELY
                                                                                                                                                                                                                                                RMDFEKMGKCIIINNKNFDKVTGMDVRNGTDKDAEALFKCFRSLGFDVVVYNDCSCAKMQ
                                                                                                                                                                                                                                                                                                             NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ 120
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                                                                                                                                                                                                                FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
                                                                                                                                                                                                                                                             DLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKL 180
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                                                                                                                           303
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84.2%;
 Last sequence update)
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BY SIMILARITY.
CASPASE-7 SUBUNIT P11.
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BY SIMILARITY
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EMBL; U67321; AAC53068.1; PEMBL; D86353; BAA19730.1; -EMBL; X13088; CAA73530.1; -EMBL; BC005428; AAH05428.1; HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                          MEROPS; C14.004; -. MGD; MGI:109383; Casp7 Interpro; IPR002398; I
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification and mapping of Casp7, a cysteine protease resembling CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."; genomics 40:86-93(1997).
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Juan T.S.-C., McNiece I.K., Argen
Copeland N.G., Fletcher F.A.;
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Eukaryota; Metazoa; (
Mammalia; Eutheria; F
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van de Craen M., Vandenabeele P.,
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MEDLINE=97236307; PubMed=9125129;
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CASP7 OR MCH3 O
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TISSUE=Skeletal muscle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION: CLEAVES AND ACTIVATES STEROL
REGULATORY ELEMENT BINDING PROTEINS (STEBPS). OVEREXPRESSION
PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).
SUBBURIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBBURIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic:
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
KIDNEY. LOW LEVELS IN SPELEEN, SKELETAL MUSCLE, AND TESTIS. NO
EXPRESSION IN THE BRAIN.
PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
SUBUNITS: PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
COP522 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
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IPR002138; ICE_p10.
IPR001309; ICE_p20.
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Rodentia;
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Best Local
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Pfam; PF00655; ICE_P20; 1.
Pfam; PF00656; ICEE_P20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0120; CASPASE_P10; 1.
PROSITE; PS50207; CASPASE_P20; 1.
Wang X., Zelenski N.G., Yang J., Sakai J., Brow Goldstein J.L.;
"Cleavage of sterol regulatory element binding CPP32 during apoptosis.";
                                                                                                                                                                                                              ICE3_CRILO
Q60431;
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CHAIN
ACT_SITE
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                                                                 SEQUENCE FROM N.A.
                                                                                                                  Cricetulus longicaudatus
Eukaryota; Metazoa; Chord
                                                                                                                                                          Apopain precursor protein) (CPP-32)
                                                          TISSUE-Brain;
                                                                                                 Cricetulus
                                                                                                                                         CASP3
                                                                                                                                                                               01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                      NCBI_TaxID=10030
                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                     01-NOV-1997
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                                                                                                                                        OR CPP32.
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                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                      35, Created)
35, Last sequence update)
41, Last annotation update)
(EC 3.4.22.-) (Cysteine protease CPP32) (Yama (Caspase-3) (CASP-3) (SREBP Cleavage activity
                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.4%;
                                                                                                      (Long-tailed hamster) (Chinese hamster)
data; Craniata; Vertebrata; Euteleostomi
ntia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1346;
Pred. No. 4.
                                                                                                                                                                                                                        PRT;
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1.4e-109;
                                    Brown
              proteins
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              (SREBPs)
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Best Local S
Matches 149
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Pfam; PF00656; ICE_p20; 1.

PRINTS; PR00376; IIIBCENZYME.

SMART; SM00115; CASC; 1.

PROSITE; PS01122; CASPASE_CYS; 1

PROSITE; PS01121; CASPASE_HIS; 1

PROSITE; PS01207; CASPASE_P10; 1

PROSITE; PS50208; CASPASE_P10; 1

PROSITE; PS50208; CASPASE_P20; 1
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PROPEP
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>-</del> --
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InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; C14.003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
     230
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nes 149; Conserv
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(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

(CASPASE LOCATION: Cytoplasmic.

PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES TO THE CATIVATE BY GRANZYME B, CASPASE-1 OF THE PROPERTIDES TO ACTIVE SUBUNITS.

AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVICE VERSA (BY SIMILARITY).

SIMILARITY: BELONGS TO PERTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O J. 15:1012-1020(1996).

FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT PROTECULY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOPHELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHENT DOMAIN. CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY). SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
                                                                                           LEFMHILTRVNRKVATEFESFSLDSTFHAKKQIPCIVSMLTKELYF
                                            LEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
                                                                                                                                                                                                NEDSVDAKPDRSSFVPSLFSKKK--KNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINN
                                                                                                                                                                                                                     CFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAI
                                                                                                                                                                                                                                                                                                                          KNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAA
                                                                                                                                                                                                                                                                                                                                                                                                      NETSVDSKSIKNFEVKTIHGSKSMDSGIYLDS---
                                                                                                                                                                                                                                                                                                   KNFHKSTGMTPRSGTDVDAAKLRETFMALKYEVRNKNDLTREEIVELMKNASKEDHSKRS
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277
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52.1%;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
APOPAIN P17 SUBUNIT.
APOPAIN P12 SUBUNIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
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Pred. No. 4.1e-57;
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBF3A4590A2828A3 CRC64;
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275
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DE Apopai
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GN CASP3
OC ELLAN
RP SEQUEN
R
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Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A., Kikly K., Winkler J.D., Sung C.M., Debouck C., Richardson S., Levy M.A., DeWolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S., Ryan M.D., Haltiwanger R.C., Liang P.-H., Janson C.A., McDevitt P., Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M., Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E., "Potent and selective nonpeptide inhibitors of caspases 3 and 7 inhibit apoptosis and maintain cell functionality.";
                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS). MEDLINE=20283632; PubMed=10821855;
                                                                                                                                                                                                                                                                                          Mittl P.R., di Marco S., Krebs J.F., Bai X., Priestle J.P., Tomaselli K.J., Grutter M.G., "Structure of recombinant human CPP32 in comptetrapeptide acetyl-Asp-Val-Ala-Asp fluoromet J. Biol. Chem. 272:6539-6547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Dir
Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,
Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thornberry N.A., Becker J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MEDLINE-96266352; Pubmed-8673606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95292347; PubMed-7774019;
Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
Beidler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.,
"Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fernandes-Alnemri T., Litwack G., Alnemri E.s
"CPP32, a novel human apoptotic protein with
Caenorhabditis elegans cell death protein Cec
                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apopain precursor protein) (CPP-32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICE3_HUMAN P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                          x-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
MEDLINE=97197830; PubMed=9045680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abelle M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (-RAY CRYSTALLOGRAPHY (2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identification and inhibition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-1 beta-converting enzyme.
J. Biol. Chem. 269:30761-30764(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95074098; PubMed-7983002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mammalian apoptosis.";
ure 376:37-43(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     three-dimensional structure of apopain/CPP32, a key mediator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81:801-809(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Struct.
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s (Human).
Metazoa; Chordata; C
Metazoa; Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicholson D.W., Fazil K.M., Peterson E.P., Rasper D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-46 AND 175-193,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7596430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32, Last sequence update
41, Last annotation upda
(EC 3.4.22.-) (Cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC 3.4.22.-) (Cysteine protease CPP32) (Yama (Caspase-3) (CASP-3) (SREBP cleavage activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3:619-625(1996)
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                                                                                                                                                                                                                                                                                                                       ketone.";
                                                                                                                                                                                                                                                                                                                                               with the
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                                                                                                          Р.Ј
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PROSITE; PS01122; CASPASE_CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20;

Hydrolase; Th 3D-structure.

Thiol

protease;

Zymogen;

Apoptosis; Polymorphism,

PRINTS; PR00376; ILIBCENZYME SMART; SM00115; CASC; 1.

Pfam; PF00655;

PF00656;

ICE_p10; 1. ICE_p20; 1.

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CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                      PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                         Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "In vitro activation of CPP32 and Mch3 by Mch4, a novapoptotic cysteine protease containing two FADD-like Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                               [nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fernandes-Alnemri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96353838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
SUBUNIT: HETERODINER OF A 17 kDa (P17) AND A 12 kDa (P12) SUB
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART,
AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND
IN TESTIS. ALSO POUND IN MANY CELL LINES, HIGHEST EXPRESSION
CELLS OF THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF PROPERTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE AUTOCATALYTY O
                                                                                                                                                                                                                                                                                                                                                          1PAU; 07-JUL-97.
1CP3; 24-DEC-97.
1GFW; 23-JUN-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND
                                                                                                                                                                                                                                                                                                   600636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLEAVAGE OF HUNTINGTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                        U13737; AAA65015.1;
U13738; AAB60355.1;
U26943; AAA74929.1;
                                                                                                                                                                                                                                                                                                                    HGNC: 1504;
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IPR001309;
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                                                                                                                                                                                                                                                                                                                       CASP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=8755496;
T., Armstrong R.
F., Fritz L.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8696339;
cholson D.W., Rasper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            institutions as long as its content
                                                                                                                                                                                                                                 ICE_p20
                                                                                                                                                                                                                                                       ICE_p10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .C., Krebs J.,
Trapani J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF CPP32 ALSO OCCUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Srinivasula S.M.,
Tomaselli K.J.,
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MBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                    Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I., Hirshfield A.N., Tilly J.L.;
"Interleukin-1 beta-converting enzyme-related proteases (IRPs) and mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa cell of the ovarian follicle.";
                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                P55213; P70543; Q62993; P97699;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity (SCA-1) (LICE) (IRP).
            SEQUENCE FROM N.A
TISSUE-Brain;
                                                                                                                                                                                     a cysteine protease
                                                                                                                      MEDLINE=96042508; PubMed=7588240;
                                                                                                                                   TISSUE-Ovary;
                                                                                                                                                                                                             Fletcher F.A.;
                                                                                                                                                                                                                       Juan T
                                                                                                                                                                                                                                MEDLINE=96358624;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                             CASP3 OR CPP32
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CHAIN
CHAIN
 MEDLINE-97184204; PubMed-9030616
                                                                                                                                           SEQUENCE OF 30-241 FROM N.A.
                                                                                                                                                                                                 Molecular characterization
                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF
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                               ovarian follicie. /
inology 136:5042-5053(1995)
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                                                                                                                                                                                                                      .S.-C., McNiece
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                                                                                                                                                                13:749-755(1996)
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                                                                                                                                                                                                                                PubMed=8761296;
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APOPAIN P12 SUBUNIT.
BY SIMILARITY.
BY SIMILARITY.
D -> E (IN ISOPORM BETA).
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                    mouse and rat interleukin-1
                                                                                                                                                                                               mouse
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                                                                                                                                                                                                                                                                                                                                                                                                 277
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7.3e-55;
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                                                                                                                                                                                                                    Gilbert D.J.,
                                                                                                                                                                                    CPP32 beta gene beta converting
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                                                                                                                                                                                                                                                                          Murinae; Rattus
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                                                                                                                                                                                                                    Copeland N.G.,
                                                                                                                                                                                   enzyme
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Pfam; PF00655; ICE_p10; I.

Pfam; PF00656; ICE_p20; 1.

PRANTS; PR00376; ILIBCENZYME.

SMART; SM00111; CASC; 1.

PROSITE: PS01122; CASPASE_CYS; 1

PROSITE: PS01121; CASPASE_HIS; 1

PROSITE: PS50207; CASPASE_P10; 1

PROSITE; PS50208; CASPASE_P20; 1
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between
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                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                 InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10
InterPro; IPR001309; ICE_p20
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protease;

Zymogen;

Zymogen; Apoptosis.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
APOPAIN P12 SUBUNIT.
APOPAIN P12 SUBUNIT.
BY SIMILARITY.
BY SIMILARITY.

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EMBL; U49930;
EMBL; U34685;
EMBL; U84410;
EMBL; U58656;
EMBL; U58656;
                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K., Rosteck P. Jr., Poirier G.G., Paul S.M.; "Cloning and expression of a rat brain interleukin-lbeta-converting enzyme (ICE) related protease (IRP) and its possible role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-264 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ADULT BRAIN.

ADULT BRAIN.

PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES FYM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CP932 ALSO OCCUR VICE VERSA (BY SIMILARITY).

VICE VERSA (BY SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT PROTEOLYTICALLY CLEAVES POLY(ADP-RIDOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-HELIX LEGGINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN. CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY). SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: EXPRESSED IN HEART,
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DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS
                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                 AAC52261.1;
AAB41792.1;
AAB02722.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cultured cerebellar granule neurons."; 17:1561-1569(1997).
                                                                                                                                       AAC52765.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
                                 . . . . .
                                                                                                                                                                                                                               utions as long as its content is in no way is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                             There are no
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Best Local
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01-NOV-1997
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CONFLICT
SEQUENCE
                                                                                                                       STRAIN=Con,....
MEDLINE=97190206; Pubmeu----
van de Craen M., Vandenabeele
van de Craen M., Schot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
SEQUENCE FROM N.A. TISSUE-Brain;
                                                                                                                                                                                                                                                                                                      activation NGF.";
                                                                                                                                                                                                                                                                                                                         MEDLINE-97224429; PubMed-9070890; MEDLINE-97224429; PubMed-9070890; Mukasa T., Urase K., Momoi M., Kimura I., Momoi T.; "Specific expression of CPP32 in sensory neurons of mouse embryos and activation of CPP32 in the apoptosis induced by a withdrawal of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Juan T.S.-C., McNiece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last annotation update)
Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, 15-JUN-2002 (Rel. 41,
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                                                                 FEBS Lett.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                Biochem. Biophys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncogene 13:749-755(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fletcher F.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=96358624; PubMed=8761296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASP3 OR CPP32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNFHKSTGMSARNGTDVDAANLRETFMALKYEVRNKNDLTREEIMELMDSVSKEDHSKRS 112
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                                                                 ization of seven murine 403:61-69(1997).
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                                                                                                                                                           PubMed=9038361;
Vandenabeele P.,
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                                                                                                                                                                                                                                                                              Commun.
                                                                                                                                   Schotte P.,
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Sciurognathi; Muridae; Murinae; Mus
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-> M (IN REF. 3).
ADABF418E2507402 CRC64;
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P., van Criekinge
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No. 1.1e-54;
82
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                                                                                     family members."
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                                                                                                                                   w.,
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                                                                                                                                   Brande I.,
Beyaert R.,
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PROSITE; PS01121; CASPASE_HIS;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U54802; AAC52768.1;
EMBL; U49929; AAC52764.1;
EMBL; D46352; BAA21727.1;
EMBL; Y13086; CAA77528.1;
EMBL; U19522; AAC53196.1;
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TISSUE SPECIFICITY: HIGHEST EXPRESS
KIDNEY AND HEART. LOWER EXPRESSION
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C -> G (IN REF. 2)
N -> T (IN REF. 2)
Q -> E (IN REF. 2)
L -> M (IN REF. 2)
L -> M (IN REF. 2)
L -> M (IN REF. 2)
Y -> F (IN REF. 2)
Y -> F (IN REF. 2)
Y -> F (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    It is produced through a collaboration
                                                                                                                                                                                                                     Apoptosis
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 CRC64;
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S IS
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Query Match Best Local Matches 14

Similarity

43.6%;

Score Pred.

Conservative

40;

Mismatches

Indels

18;

Gaps

703;

DB 1; 4e-53;

Length 277;

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RESULT
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PRINTS; PROUL
SMART; SMOOLLS; CAS
                                                                                                                                                                                                                                                                                                                                                             Yaoita Y., Nakajima K.;

"Induction of apoptosis and CPP32 expression by thyroid hormone in a myoblastic cell line derived from tadpole tail.";

J. Biol. Chem. 272:5122-5127(1997).

-i- FUNCTION: IMPORTANT MEDIATOR OF APOPTOSIS. AT THE ONSET OF APOPTOSIS IT PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|-GLY-217 BOND (BY SIMILARITY).

-i- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12)
                                                   Pfam; PF00655;
Pfam; PF00656;
                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                  +:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XENLA
                                                                                                                        MEROPS; C14.003;
                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=97184166;
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01-NOV-1997 (Rel. 35,
15-JUN-2002 (Rel. 41,
                                                                                InterPro;
                                                                                             InterPro;
                                                                                                          InterPro;
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ween the Swiss Institute of Bioinformatics and the
European Bioinformatics Institute. There are no re-
by non-profit institutions as long as its conten
                                                                                                                                                                                                                                                                                     OTHER CASPASES (BY SIMILARITY). SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
MISCELLANEOUS: THE SUBUNITS ARE DERIVED FROM THE PRECURSOR SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM AND PROBABL OTHER CASPASES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAI 195
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                                                                                                                                  D89784; BAA14018.1;
P42574; IPAU.
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                                    F00655; ICE_p10; 1.
F00656; ICE_p20; 1.
PR00376; IL1BCENZYME
                                                                              IPR002138; ICE_p10
IPR001309; ICE_p20
                                                                                                         IPR002398; ICE.
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            CASPASE_CYS;
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Last annotation updat
3.4.22.-) (Cysteine p
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ICE1_SPOFR
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Best Local S
Matches 146
               use by modified
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PROSITE; PS
PROSITE; PS
Hydrolase;
PROPEP
CHAIN
                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                           cleaves the nuclear immunophilin FKBP46, is the target of the baculovirus antiapoptotic protein p35.;
J. Biol. Chem. 272:1421-1424(1997).
-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION (BY SIMILARITY). INHIPTHE BACULOVIRUS ANTI-APOPTOTIC PROTEIN P35. CLEAVES P35. NUCLEAR IMMUNOPHILIN FKBP46.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=97153084; PubMed=8999805;
Ahmad M., Srinivasula S.M., Wang L., Litwack G.,
                                                                                                                                                                                                                                                                                                                                                                                                                               ICE1_SPOFR P89116;
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Olitrysia; Noctuoidea; Noctuoidea; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-1 precursor (EC 3.4.22.-)
                                                                                                                                                                                                                                                                                                                                                              Spodoptera frugiperda (Fall armyworm)
                                                                                                                                                                                                                                                 Alnemri E.S.
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7108;
                                                                                                                                                                                                                     alnemri E.S.;
"Spodoptera frugiperda caspase-1, a novel insect
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                                                                                       PTM: AN AUTOCATALYTIC MECHANISM GENERATES TH SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                SUBUNIT: HETERODIMER OF
                                                                                                                   SUBUNIT.
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requires a license
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PS50207;
PS50208;
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282
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CASPASE_P20;
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282 A
131 B
174 B
32124 MW;
license agreement (See http://www.isb-sib.ch/announce/
                          institutions as long
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               is not removed.
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APOPAIN P12 SUBUNIT.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                               RESULT 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 122;
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ACT_SITE
SEQUENCE
                                                                                                                              O01382; Q9VAH1;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase precursor (EC 3.4.22.-) (drICE).
ICE OR CG7788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
CHAIN
 Fraser A.G., Eva
"Identification
             TISSUE-Embryo;
MEDLINE-97327558; PubMed-9184225;
                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Musconpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00655; ICE_p10; Pfam; PF00656; ICE_p20; SMART; SM00115; CASC; 1
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InterPro;
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                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                        ICE_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                ASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRGMAIIFNHEHFD-IHSLKSRTGTNVDSDNLSKVLKTLGFKVTVFPNLKSEEINKFIQQ
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IPR001309;
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            Evan
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40.5%;
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Drosophila melanogaster ICE/CED-3-related
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POTENTIAL.
CASPASE-1 SUBUNIT P12.
BY SIMILARITY.
BY SIMILARITY.
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2; Mismatches
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Pred. No. 1
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dutbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Kimmel B.E., McIntosh T.C., McLeod M.P., McPherson D.,
RA McHalov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Shong F. W., Zhong W., Zhou X., Zhu S., Zho Q.A.,
RA Wang Z.-Y., Shong F. W., Shon M., Zhong G., Zheo Q., Zheng L.,
RA Sheng X.H., Zhong F. W., Shon M., Zhou X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA Gibs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA Gibs R.A., Myers E.W., Rubin G.M., Land G.M., Shong G., Zho Q., Zheng L.,
RA Shore G. W., Zhou X., Smith H.O.,
RA
                                  Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME
                    PRINTS; PR00376
SMART; SM00115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshako
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y12261; CAA72937.1; ... EMBL; AE003771; AAF56939.1;
                                                                                                                                                                                                                                                                           or send
                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
  PROSITE; PS01122;
                                                                                                                                                           FlyBase; FBgn0019972; Ice.
                                                                                                                                                                             MEROPS; C14.015;
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                                                                                                 InterPro;
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EMBO J. 16:2805-28
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                                                                                             : IPR002398;
: IPR002138;
: IPR001309;
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                      CASc;
CASPASE_CYS;
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                                                                                             ICE_p10.
ICE_p20.
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institutions as long as its content
                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
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Henderson S.N.,
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Matches
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002002; 09W1N0;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                           Science [2]
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ACT_SITE
CONFLICT
CONFLICT
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R. George R.A., Lewis S.E., Richards S., Ashbourner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer
                                                  STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                   DROME
                                                                                                                                                                                                     TISSUE-Embryo
                                                                                                                                                                                                                                     Muscomorpha; Ephydroidea;
NCBI_TaxID=7227;
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    McCall K., Steller H.;
    a Drosophila cell death protease essential for development.";
    nce 275:536-540(1997).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSYRKNVA----KMVTDR-HAAEYNMRHKNRGMALIFNHEHFE-VPTLKSRAGTNVDCEN 121
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                                                                                                       McCall K., Steller 277:167-167(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50208;
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CASPASE_P10;
CASPASE_P20;
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BY SIMILARITY.
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BY SIMILARITY:
CASPASE SUBUNIT P12 (
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A -> S (IN REF: 1).
S -> T (IN REF: 1).
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Pred. No. 2
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.8e-39;
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PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_HIS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
PROSITE; PS50208; CASPASE_P20; 1.

Apoptos1s

Pfam; PF00655; ICE_p10; 1. Pfam; PF00656; ICE_p20; 1. InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10
InterPro; IPR001309; ICE_p20

FlyBase; FBgn0010501; MEROPS; C14.016; HSSP; P42574;

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RA FOSIER C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

AHarris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

AHarris N.L., Harvey D., Heiman T.J., Wei M.-H., IDegwam C.,

AHarris N.L., Harvey D., Heiman T.J., Wei M.-H., IDegwam C.,

AHAR Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

AKIMMEL B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

ALIU X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

AHAR Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

AHAR Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

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"The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).

-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION (BY SIMILARITY).

PROTECLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). LOSS OF ZYGOTIC DCP-1 FUNCTION CAUSES LARVAL LETHALITY AND MELANOTIC
                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-s
EMBL; AF001464; AAB58237.1; EMBL; AE003461; AAF47027.1;
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Durbin K.J., Evangelista C.C., Ferraz C.,
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Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier
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                                                                                                                                                                                                       equires a license agreement (Semail to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-6 precursor (EC 3.4.22.-) (Apoptotic
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Mammalia; Eutheria;
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                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG,
TESTIS, AND HEART. LOWER LEVELS IN SPLEEN, SKI
                                                                                                                                                                                                                                                                                FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE) POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).

SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED CONTROL OF A 18 kDA (P18) AND A 11 kDA (P11) SUBUNITED CONTROL OF A 18 kDA (P18) AND A 11 kDA (P11) SUBUNITED CONTROL OF A 18 kDA (P18) AND A 11 kDA (P11) SUBUNITED CONTROL OF A 18 kDA (P18) AND A 11 kDA (P11) SUBUNITED CONTROL OF A 18 kDA (P18) AND A 11 kDA (P11) SUBUNITED CONTROL OF A 18 kDA (P18) AND A 11 kDA (P11) SUBUNITED CONTROL OF A 18 kDA (P18) AND A 11 kDA (P11) SUBUNITED CONTROL OF A 18 kDA (P18) AND A 11 kDA (P11) SUBUNITED CONTROL OF A 18 kDA (P18) AND A 11 kDA (P18
                                                                                                                 SUBUNITS (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                        (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQ-SDDPHFHEKKQIPCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRDILKHVGKAAELDHTDNDCLAVAILSHGEHGYLYAKDTQYKLDNIWHYFTATFCPSLA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYNNNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMLTRILRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMLTKELYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NINNGSWYMQSLIRELNANGKKYDLLTLLTEVNQRVALDFESNVPATPMMDRQKQIPCLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKPKLFFIQACQGDRLDGGITLEKG-VTETDGESSTSYKIPIHADFLFSYSTIPGYFSWR
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                                                                                                                                                                                                                                                                  SIMILARITY)
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    non-profit institution and this statement is
                                                                                                                                                             CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE
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215
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196
35926 N
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W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 532.5; DB 1
Pred. No. 9.5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Y SIMILARITY.
B5FF0FF75EB8E2BD CRC64;
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P., van Criekinge
    removed.
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                  There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                AND A 11 kDa (P11) SUBUNIT
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Usage
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inge W., Beyaert R.,
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  and
                                                          EMBL outstation
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                                                                             a collaboration
  for
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Best Local :
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Pfam; PF00656; ICE_P20; 1.

PRINTS; PR00376; ILIBCENZYME.

SMART; SM00115; CASC; 1.

PROSITE; PS01122; CASCASE_HIS; 1.

PROSITE; PS01121; CASCASE_HIS; 1.

PROSITE; PS01121; CASCASE_HIS; 1.

PROSITE; PS01727; CASCASE_P10; 1.

PROSITE; PS01028; CASCASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                      01-OCT 1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-6 precursor (EC 3.4.22.-) (Apoptotic
                                                            TISSUE=T-cell
                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                CASP6 OR MCH2
                                                                                                                                                                                                           ICE6_HUMAN P55212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP
                    MEDLINE-95316841; PubMed-7796396; Rernandes-Alnemri T., Litwack G., Alr
Meh2, a new member of the apoptotic
                                                                      SEQUENCE FROM N.A.
            family
                                                                                                NCBI_TaxID=9606
                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROPEP
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InterPro; IPR001309;
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                                                                                                                                                                                                                                                                                                                                                         227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         116
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                                                                                                                                                                                                                                                                                  QVPCFASMLTKKLHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CAKMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAEQYKMDHKRRGVALIFNHERFFWHLTLPERRGTNADRDNLTRRFSDLGFEVKCFNDLR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS 115
                                                                                                                                                                                                                                                                                                         QIPCVVSMLTKELYF
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99; Conserv
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1 5
6 162
163 176
177 276
104 104
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276
55:2737-2742(1995)
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                                                                                                            Chordata;
Primates;
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38.8%;
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BY SIMILARITY.
CASPASE-6 SUBUNIT F
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 483.5; DB 1;
Pred. No. 1.3e-34;
3; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CASPASE-6 SUBUNIT P11
                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                        PRT;
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                                    Alnemri E.S.
                      Ced-3/Ice cysteine
                                                                                                                                                                                                                        293
                                                                                                                                                                                                                        B
                                                                                                                                                          protease Mch-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P18
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                      protease
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Best Local
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InterPro; IPR002138; ICE_p10.
InterPro; IPR002139; ICE_p20.
InterPro; IPR001309; ICE_p20; 1.
Pfam; PF00655; ICE_p10; 1.
PfANTS; PR00376; ILEE_D20; 1.
PRINTS; PR00376; ILBECENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                           ACT_SITE
ACT_SITE
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS0112; CASPASE_CYS;
PROSITE: PS01121; CASPASE_HIS;
PROSITE: PS50207; CASPASE_P10;
PROSITE: PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Biol. Chem. 271:27099-27106(1996).
-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASE RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-R POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROGRAMMED CELL DEATH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 601532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
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MEDLINE=97059171; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Srinivasula S.M., Fernandes-Alnemri T. Armstrong R.C., Wang L., Trapani J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROCESSING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 11 kDa SUBCELLULAR LOCATION: CYTOPLASMIC.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOF SEEM TO HAVE PROTEOLYTIC ACTIVITY.

PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
EKPKLEFIQACRGTE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copy
een the Swiss Institute
                                                                     AEELLLKIHEVSTVSHADADCFVCVFLSHGEGNHIYAYDAKIEIQTLTGLFKGDKCHSLV
                                                                                                               CAKMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLL 175
                                                                                                                                                           PAEKYKMDHRRRGIALIFNHERFFWHLTLPERRRTCADRDNLTRRFSDLGFEVKCFNDLK
                                                                                                                                                                                                     PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U20536; AAC50168.1;
U20537; AAC50169.1;
P42574; IPAU.
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                                                                                                                                                                                                                                                                                                                                                293 AA;
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163
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Fernandes-Alnemri T.,
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193
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37.9%;
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                                                                                                                                                                                                                                                     42;
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                                                                                                                                                                                                                                                                                                                                                              CASPASE-6 SUBUN
BY SIMILARITY.
BY SIMILARITY.
MISSING (IN ISC
                                                                                                                                                                                                                                                 Score 466; DB 1;
Pred. No. 4.7e-33;
2; Mismatches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CASPASE-6 SUBUNIT
    *LDDAIQADSGPINDTDANPRYKIPVEADFLFAYST
                                                                                                                                                                                                                                                                                                                                           ISSING (IN ISOFORM BETA)
BD9204E23CE1F670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zymogen; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND A 11 kDa (P11) SUBUNIT
                                                                                                                                                                                                                                                     107;
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BETA ISOFORM DO
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                         225
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LCEB_HUMAN STANDARD; PRT; 479 AA.

AC Q14790; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796; Q15780;

AC Q15806; Q9UQ81; Q14676;

DT Q1-NOV-1997 (Rel. 35, Created)

DT Q1-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)

DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-

DE like protease) (FADD-like ICE) (FIICE) (Apoptotic cysteine protease)

CASP8 OR MCH5.
  ALD DACCOCK DEED DOTT ACCOCK OCCOCK DEED DOTT ACCOCK DE DOTT 
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ICE8_HUMAN
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                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-99132295; PubMed=99
Grenet J., Teitz T., Wei T.
"Structure and chromosome 1.
Gene 226:225-232(1999).
[5]
                                                               Fernandes-Alnemri T., Croce C.M., Litwack (Armstrong R.C., Alnemri E.S.; FADME-1, a novel FADD-11ke anti-apoptotic Fas/TNFR1-induced apoptosis.", J. Biol. Chem. 272:18542-18545(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzio M., Chinnaiyan A.M., Kischkel F.C., O'Rourke K., Sl
Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann
Krammer P.H., Peter M.E., Dixit V.M.;
"FLICE, a novel FADD-homologous ICE/CED-3-like protease,
to the CD95 (Fas/APO-1) death-inducing signaling complex
Cell 85:817-827(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96353838; PubMed=8755496; Fernandes-Alnemri T., Armstrong R. Wang L., Bullrich F., Fritz L.C., Litwack G., Alnemri E.S.;
                                                                                                                                                                                    MEDLINE-97373543;
Srinivasula S.M.,
                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptotic cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D "Involvement of MACH, a novel MORTI/FADD-interacting Fas/APO-1- and TNF receptor-Induced cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Thymus, and B-cell; MEDLINE=96279826; PubMed=8681376;
PARTIAL SEQUENCE,
MEDLINE-97121412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "In vitro activation of CPP32 and Mch3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-T-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96279827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85:803-815(1996).
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                                                                                                                                                                                                                                                                                                      PubMed=9931493;
T., Wei T., Valentine
romosome localization
                                                                                                                                                                                                                                                                                                                                                                                                          e protease containing two FADD-like domains. Sci. U.S.A. 93:7464-7469(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8681377
                                                                                                                                                                                                            PubMed=9228018;
  AND PROCESSING PubMed=8962078;
                                                                                                                                                                                    Ahmad M.,
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                                                                                                                                                                                    Ottilie
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nn M.,
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St.
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"FLICE is activated by association with the CD95 death-inducing signaling complex (DISC).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1 protease Mch5 is a CrmA-inhibitable protease that activates multiple Ced-3/ICE-like cysteine proteases.";
Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure 7:1125-1133(1999).
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Medema J.P., Scaffidi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97160607; PubMed=9006941; Muzio M., Salvesen G.S., Dixit V.
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Alnemri E.S.;
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PTM: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH THE DISC, WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B & CASPASE-10 CAN BE INVOLVED IN THESE PROCESSING EVENTS.

SIMILARITY: BELONGS TO PETTIDASE FAMILY C14.

SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
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                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECRUITS IT TO EITHER RECEPTORS. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN LIBERATED FROM THE DISC AND FREE TO ACTIVATE DOWNSTREAM APOPTOTIC PROTEASES. PROTEOLYTIC FRACKENTS OF THE N-TERMINAL PROPEPTIDE (TERMED CAP3, CAP5 AND CAP6) ARE LIKELY ETALNED IN THE DISC. CLEAVES AND ACTIVATES CASPASE 3, -4, -6, -7, -9, AND -10. MAY PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS. PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). HYDROLYZES THE SMALL-MOLECULE SUBSTRATE, AC- ASP-GLU-VAL-ASP-|-AMC. LIKELY TARGET FOR THE COMPON VIRUS CRMA DEATH INHIBITORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPHA,/MCH5-BETA, 3-ALPHA, 4-ALPHA, 1-BETA, 2-BETA, 3
BETA; ARE PRODUCED BY ALTERNATIVE SPLICING
TISSUE SPECIFICITY: ALPHA 1 AND BETA 1 ISOFORMS ARE
WIDE VARIETY OF TISSUES. HIGHEST EXPRESSION IN PERIP
LEUKOCYTES, SPLEEN, THYMUS, AND LIVER. BARELY DETECT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
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X98173;
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                                                                                                                                                                                                                                                                                                                             and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                non-profit institutions as long
                                                                                                                                                                                                                                                    email to license@isb-sib.ch).
                                                                                                   CAA66853.1;
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InterPro; IPR001309; ICE_p20
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Pfam; PF00656; ICE_p20; 1.
Pfam; PF01335; DED; 2.
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AF102146; AAD24962.1;

J; AF10219; AAD24962.1;

J; AF102140; AAD24962.1;

J; AF102141; AAD24962.1;

J; AF102142; AAD24962.1;

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MISSING (IN ISOFORM 1 BETA).
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ERSSSLEGSPDEFSNGEELCGVMTISDSPREQDSESO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CASPASE-8 SUBUNIT P18
                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN ISOFORM 4 ALPHA)
                                                                                                                                                                                                                                                           7A5FEAA6B39B582F
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFHFCRMSWAEANSQCQTQSVPFWRRVDHLLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zymogen; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                  BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA)
                                                                                                                                                                                                      .7e-29;
                                                                                                                                                                                                                                                                                                                                               ISOFORM 3
                                                                                                                                                                                                                                                                                                                                                                             FGNVFSWW (IN ISOFORM 3
                                                                                                                                                                                                                        DВ
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                                                                                                                                                                                        114;
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2 AND
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                                                                                                                                                                                                                    Length
                                                                                                                                                                                      Indels
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                                                                                                                   -YQMKSK
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                                                                                                                                                                                   Gaps
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
             "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1 protease Mch5 is a CrmA-inhibitable protease that activates multiple
                                                                                                                                                                                                                                           "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2, and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2) critical region at chromosome 2q33-q34: candidate genes for ALS2."; Genomics 71:200-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM A). MEDLINE-21100893; PubMed-11161814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Thymus, and Spleen;
MEDLINE-99214592; PubMed-10187817;
Ng P.W., Porter A.G., Janicke R.U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97197836; PubMed=9045686; Vincenz C., Dixit V.M.; "Fas-association"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "In vitro activation of CPP32 and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two FADD-like domains."; Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                     Srinivasula S
Alnemri E.S.;
                                                                                                                                                                                                                                                                                                                                                                                   Hadano S., Yanagisawa Y., Skaug J.,
Martindale D., Koop B.F., Scherer S.
Ikeda J.-E., Hayden M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoforms of caspase-10.";
J. Biol. Chem. 274:10301-10308(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and characterization
isoforms of caspase-10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fernandes-Alnemri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96353838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CASP10 OR MCH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterleukin-1B-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461
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, Bullrich F., Fr
G., Alnemri E.S.
                                                                                                                                                                                 SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FLICE2),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FLICE2), an ICE/Ced-3 homologue, p55-mediated death signaling.";
                                                                                                                    S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272:6578-6583(1997).
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IT., Armstrong R.O., Fritz L.C.,
                                                                                                                       Ahmad M.,
                                                                                                                                                      Pubmed=8962078;
                                                                                                                                                                                    AND PROCESSING.
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Catarrhini;
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Trapani J.A.,
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RT Ced-3/ICE-like cysteine proteases.";

RI Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).

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PROSITE; PS01121; CASPASE_HIS;
PROSITE: PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
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SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
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AB038973; BAB32554.1;
AB038974; BAB32554.1;
AB038975; BAB32554.1;
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; IPR002138; ICE_p10.
; IPR003309; ICE_p20.
00655; ICE_p10; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ICE_p20; 1.
; DED; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; BAB32554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1QDU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAB32554.1;
                                                                                                                                                                                                                                                                                                                                                                                 protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILIBCENZYME
                                                                                                                                                                                                                                                                                                                                                                                                            DED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DED.
                                                                                                                                                                                                                                                                                                                                                                              Apoptosis;
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JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                           CASPASE-10
CASPASE-10
DED 1.
QPAFTLRKKLVFPVPLDALSI (IN ISOFORM B).
GNRATNGAPSLVSRGMQGASANTLNSETSTKRA -> EGSC
VQDESEPQRPLCHCQQPQLYLPEGQTRNP (IN ISOFORM
                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
MISSING (IN SHORT ISOFORM)
                                                                                MRRWSSVS -> HEDILSILTAVNDDVSRRVDKQGTKKQMP
                                                                                                      MLKFLEKTMEIRGRKRTVWGAKQISATSLPTAISAQTPRPP
                                                                                                                                                                                                                                                                                                                                                                           Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no
                                                                                                                                                                                                                                                                       SUBUNIT P23/17.
                                                                                                                                                                                                                                                                                                                                                                           Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration -
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Searc	Qу	Db .	Qу	Qy Db	D Qy	Db Qy	. Que Bes Mat	SO FT FT FT
Search completed: December Job time : 11.4483 secs	287 QIPCVV : :: 469 LVPRML	227 PGYYSW : 444 PGYVSF	169 DRCKTL : 384 LQCPRL	111 YNDCSC : :: 324 HNNVTK	51 TRDRVF : 269 STKRAF	11 QGVEDS : 209 QGEEEI	Query Match Best Local Similarity Matches 95; Conser	VARSPLIC CONFLICT CONFLICT CONFLICT SEQUENCE
: Decemb 83 secs	QIPCVVSMLTKEL 299 : :: : LVPRMLKFLEKTM 481	RSPGRGSW RHVEEGSW	LEKPKLFF AEKPKLFF	AKMQDLLKI : : : : VEMEMVLQI	TYQYNMNE : VYRMNRNH	SANEDSV :: VSQTDVKT	th 24. Similarity 30. 95; Conservative	274 68 268 410 521 AA;
	299 481	PGYYSWRSPGRGSWFVQALCSIL	EKPKLFFIQACRGTELI 	(KAS-EEDH! - KQKCNPAH!	EKLGKCII : RGLCVI	QGVEDSANEDSVDAKPDRS	90 96 00 00	521 1 68 268 410 58950 MW;
2, 2002, 12:56:29		PGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKK 	DRCKTLLEKPKLFFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTV :	YNDCSCAKMODLLKKAS-EEDHTNAACFÁCILLSHGEENVIYGKD-GVTPIKDLTAHFRG : : : : : : : : : :	TRDRVPTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIV:	OGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKT		< ⊣ਰੜ
: 29		MQILTRVND	PINDTDA ; ALNPEQAPT	LLSHGEENVI : : :ILTHGRFGAV	GMGVRNGTD:	GNRATNGAP	ю В	ISSING (IN ISOFORM C)> G (IN REF. 2)> A (IN REF. 3)> I (IN REF. 3). 840348AE502B8243 CRC6
		RVARHFESQ	NPRYKIPVE : : SLQDSIPAE	YGKD-GVTP : YSSDEALIP)KDAEALFKC KDAEILSHV	SFVPSLFSKKKKNVTMRSIKT : : : :: : RATNGAPSLVSRGMQGASANTLNSET	l; Length 521; 26; 99; Indels	ORM C). 2). 3). 3). 3). 43 CRC64;
		SDDPHFHEKK	ADFLFAYS:	PIKDLTAHFI ::: : PIREIMSHFT	FRSLGFDV - FQWLGFTVI	WTMRSI ; ;; ;ASANTLNS;	64;	
		KK 286	rv 226 rv 443	RG 168 TA 383	IV 110 : HI 323	KT 50 :1 ET 268	Gaps	
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Result
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                           720.5
719
623.5
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                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                    d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 2000000000
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  44.6
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1613
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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sp_rvirus:*
                                                                                                                                                                                                                                                                                                                                                                                                                      sp_vertebrate: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_rodent:*
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                                                                                                                                                                                                                                        Length DB

    2, 2002, 12:54:49; Search time 28.7328 Seconds
(without alignments)
    2172.860 Million cell updates/sec

                                                      Q9I8S9
077623
 Q9BQE7
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Q95ND5
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093415
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                        093415 gallus gall
091b56 xenopus lae
091859 oncorhynchu
077623 ovis aries
099m47 mus musculu
035397 rattus norv
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Q95nd5 sus scrofa
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Q9ib65 xenopus lae
Q98ui8 brachydanio
Q93417 gallus gall
Q9bqe7 homo sapien
Q9d089 mus musculu
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
252	255	255.5	275.5	284	284	305	305	. 305	309	314.5	317	356.5	362	364.5	371.5	372.5	377.5	396	411.5	414.5	423.5	425.5	443	444.5	446	446	446.5	447.5
15.6	15.8	15.8	17.1	17.6	17.6	18.9		•	•	•	•	•	22.4		23.0				25.5	•			٠	27.6	•	27.7	27.7	27.7
339	347	450	393	536	268	826	452	263	423	417	435	416	500	454	520	403	454	476	326	399	496	538	482	479	308	308	482	480
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Q8TDI3	Q9GV89	Q9XYF4	Q9R0S9	018203	Q9TZP6	Q9Y055	055194	Q9TZP5	Q9IB67	091106	Q9BUP7	Q9вQ62	Q9IB64	О∂ЛНК1	Q9IB62	Q90WU0	Q9R0T0	Q918J3	Q9GV88	Q9IB63	Q9C0K4	Q8TDI5	Q9JHX4	Q8WYQ8	Q9VET9	Q9NHF9	Q90WU1	089110
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ALIGNMENTS

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088550
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 Query Match
Best Local Similarity 84.9
Matches 256; Conservative
                                                                                                                 InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR0011309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
                                                PROSITE; PS01122; CASPASE_CYS; PROSITE; PS01121; CASPASE_PIS; PROSITE; PS50207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20; SEQUENCE 303 AA; 34324 MW;
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                    088550;
                                                                                                                                                                                                                                    "Rat caspase-7 sequence.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF072124; AAC24011.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                           Forghani F.,
                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                   Caspase-7
                                                                                                                                                                                                             MEROPS; C14.004;
                                                                                                                                                                                                                         ISSP; P42574;
                                                                                                                                                                                                                                                               "Rat caspase-7
                                                                                                                                                                                                                                                                                          TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           Roy S.;
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             86.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
 Score 1395; DB 11;
Pred. No. 1.3e-119;
1; Mismatches 26;
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A71728754BF199DD CRC64;
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1 MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY 60

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RESULT

Q91B65

ID Q92B65

O07 O17 O17

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                                                                                                                                                            Query Match
Best Local Similarity
Matches 196; Conserv
                                                                                                                                                                                                                                                  Pfam; PF00655; ICE_p10; 1.

Pfam; PF00656; ICE_p20; 1.

PFINTS; PR00376; ILIBCENZYME.

SMART; SM00115; CASC; 1.

PR0SITE; PS01122; CASPASE_CYS; 1.

PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.

PROSITE; PS0207; CASPASE_P10; 1.

PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20209426; Pubmed-10744739; MEDLINE-20209476; Pubmed-10744739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9IB65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB038170;
HSSP; P42574; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; (
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ממאקן אוום מ., Takahashi A.,
"Structure, expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XCASPASE-7
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NVGRCIIINNKIFDKITGMGARNGTDIDARELLRCFKGLGFDVNVYNNKSCEEMENLLRT
                      DEPRPEEEEGEDSVDAKPDRSQRFSIFSSTKKKKVEDKPPKTNNNVRIVTPAFQYKMNNG
                                                                                                  EEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKT---TRDRVPTYQYNMNFE
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0 (TrEMBLrel. 15,
2 (TrEMBLrel. 20,
                                                                                                                                                                                                                                      318
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPAU.
                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275:10484-10491(2000)
BAA94748.1; -.
                                                                                                                                                                                                                                      35937 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ican clawed frog).
Chordata; Craniata; Ve;
; Anura; Mesobatrachia;
                                                                                                                                                                              63.5%;
                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function
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                                                                                                                                                    Score 1025; DB 13
Pred. No. 1.1e-85;
3; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence up
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                                                                                                                                                                                                                                      6EBC6684AF86A128 CRC64;
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Best Local S
Matches 147
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01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01122; CASPASE_CYS;
PROSITE; PS01121; CASPASE_HIS;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
SEQUENCE 282 AA; 31522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB047003; BAB32409.1; -. HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002398;
InterPro; IPR002138;
InterPro; IPR001309;
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                      SPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVS
                                                                      NTMTGSWFIQSLCEMMTKYGSELELLQIMTRVNHKVALDFESTSNMPGFDAKKQIPCIVS
                                                                                                                                                   KMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEK
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147; Conserv
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ICE_p20.
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nd Gene Expression
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Last sequence up
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Pred. No. 4.0
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hes 67;
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Best Local Similarity
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SMART; SM00115; CASC; 1.
SMART; SM00115; CASC; 1.
PROSITE; PS01121; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_PIO; 1.
PROSITE; PS02007; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
SEQUENCE 283 AA; 31675 MW; 16
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Biol. Reprod. 62:305
EMBL; AF083029; AAC3;
EMBL; B42574; 1PAU.
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093417;
01-NOV-1998
01-NOV-1998
01-MAR-2002
  O96AN1 PRELIMINARY;
O96AN1;
O1-DEC-2001 (TrEMBLrel.
O1-DEC-2001 (TrEMBLrel.
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Gallus gallus (Chicken).
Eukaryota, Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-20149872; Pubmed-10684799;
Johnson A.L., Bridgham J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells.
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NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                              CFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRV-PTYQYNMNFEKLGKCIIINN 75
                                                                                                                                                                                        LELMQILTRVNRRVA-EYESCSTRQDFNAKKQIPCIVSMLTKEFYF 28:
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PF00656; ICE_p20; 1.
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IPR002138; ICE_p10
IPR001309; ICE_p20
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9; AAC32602.1; -.
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Neognathae; Galliformes; Phasianidae; Phasiani
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Created)
Last sequence update)
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Pred. No. 6.4e-60;
4; Mismatches 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
           SEQUENCE FROM N.A.

MEDILINE-21334413; PubMed-11440638;

Muneta Y., Shimojima Y., Mori Y.;

"Porcine caspase-3: cloning and its activity during porcine PK15 cells induced by porcine Fas-ligand.";

J. Interferon Cytokine Res. 21:409-415(2001).

EMBL; AB029345; BAB55544.1; -.

MEROPS; C14.003; -.

InterPro; IPR002138; ICE_P10.
                                                                                                                                                                                                                                                    Q95ND5;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00655; ICE_p10; 1.

Pfam; PF00656; ICE_p20; 1.

PFANNTS; PR00376; ILIBCENZYME.

PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.

PROSITE; PS01212; CASPASE_HIS; UNKNOWN_1.

PROSITE; PS50207; CASPASE_P10; 1.

PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                         01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                               Q95ND5
                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                Sus scrofa (Pig).
                                                                                                                                                                                                             Caspase-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 277 AA; 31608 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 InterPro; IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC016926; AAH16926.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, La Hypothetical 31.6 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002398; ICE_pl0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LYMPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   233
                                                                                                                                                                                                                                                                                                                                                                                                                                    199
                                                                                                                                                                                                                                                                                                                                                                                                                                                             116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       თ
                                                                                                                                                                                                                                                                                                                                                             MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
                                                                                                                                                                                                                                                                                                                                                MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                                                                                                                                                                                                                                                                                     CVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKSTGMTSRSGTDVDAANLRETERNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDSVDAKPDRSSFVPSLESKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                                                                                                                                                                                       SGVDDDMAC----HKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEF
                                                                                                                                                                                                                      1 (TrEMBLrel. 19,
1 (TrEMBLrel. 19,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                              Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
ICE_p10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.7%; Score 721; DB 4; 50.9%; Pred. No. 6.4e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2F35CD3BCF7FF64A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                              277
                                                                                                                                                                                                                                                                              A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 277;
                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                  apoptosis
                                                                                                                                                                  Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                    of.
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ICE_p10;

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RESULTION OF THE CONTROL OF THE CONT
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Query Match
Best Local Similarity
Matches 146; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 144
                                                                                InterPro; IPR002398; ICE_pl0.
InterPro; IPR002138; ICE_pl0.
InterPro; IPR002138; ICE_pl0.
InterPro; IPR001309; ICE_pl0.
Pfam; PF00655; ICE_pl0; 1.
Pfam; PF00656; ICE_pl0; 1.
PFRNTS; PR00376; ILIBCENZYME.
PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
PROSITE; PS0207; CASPASE_Pl0; 1.
PROSITE; PS50208; CASPASE_Pl0; 1.
SEQUENCE 277 AA; 31642 MW; 6162767B0D2DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96KP2;
                                                                                                                                                                                                                                                                                                             "Control of the activation of the procaspase-3 by a sequence at the N-terminus of the p17 subunit.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ413269; CAC88866.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
Vallette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Oliver L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caspase-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CASP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q----KIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAALKQYVHKLELMHILTRVNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKIFGTNGPVDLKKLTSFFRGDCCRTLTGKPKLFIIQACRGTELDCGIETDSGTEDDMAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQADSGPINDTDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTSVDSKSIKTLETKILHGSKSMDSGISLDVSYKMDYPEMGLCIIINNKNFDKNTGMACR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKNVTMRSIKTTRDRV-------PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O0656; ICE_P20; 1.
PS01121; CASPASE_CYS; UNKNOWN_1.
PS01121; CASPASE_HIS; UNKNOWN_1.
PS01207; CASPASE_P10; 1.
PS50207; CASPASE_P20; 1.
PS50208; CASPASE_P20; 1.
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      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA; 31379 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
                   44.6%;
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      48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
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Pred. No. 7.1e
41; Mismatches
Score 719; DB 4;
Pred. No. 9.8e-58;
8; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                   1.
6162767B0D2DE021 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616C0F56141B012B
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nes 74;
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                                       Length 277;
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  Indels
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20;
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                                                                                                                                                                                                                                                                                                                                                                                located
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULTA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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                                                                                                                                                                                                                                                   Query Match
Best Local Sin
Matches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; C14.003; -...
MGD; MGI:107739; Casp3; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR0021309; ICE_p20.
InterPro; IPR0013109; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE: PS01122; CASPASE_CYS; 1
PROSITE: PS01121; CASPASE_HIS; 1
PROSITE: PS50207; CASPASE_P10; 1
PROSITE: PS50208; CASPASE_P20; 1
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01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                     Protease.
NON_TER
SEQUENCE
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"Multiple Pathways of Apoptosis Converging on Submitted (JUL-1996) to the EMBL/GenBank/DDBJ EMBL; U63720; AAD09504.1; -.
HSSP, P42574; 1PAU.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9QWI4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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                             202
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                                                                                                                                                                                 82 TGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFACIL 141
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INDTDANPR-YKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQ
                                                               LSHGDEGVIYGTNGPVELKKLTSFFRGDYCRSLTGKPKLFIIQACRGTELDCGIETDSG-
                                                                                             LSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQADSGP
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24; Conservative
                                                                                                                                                                                                                                                                                                                                       220
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(TrEMBLrel. 13, Last sequence up)
(TrEMBLrel. 21, Last annotation
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                     W.
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                                                                                                                                                                                                                                              Score 623.5;
Pred. No. 4e-4
29; Mismatches
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                     FE7F4857C4EBA544 CRC64;
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No. 4e
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4e-49;
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                                                                                                                                                                                                                                          PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
SEQUENCE 304 AA; 34534 MW; 51
                                                                                                                                                                                                                                                                                                                                                                                243
                                                                                                                                                                                                                                                                                                           Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                            InterPro; IPR002398; ICE_p10.
InterPro; IPR001309; ICE_p20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-20149872; PubMed-10684799;
Johnson A.L., Bridgham J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caspase-6
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                          181
                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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                                                192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11953316
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QALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
                     DDPVLVQDSVDSKDETTVNQTEVDAAGVYTLPAGADFIMCYSVAQGYFSHRETVNGSWYI 240
                                                DDAI - - - - -
                                                               SNADCFVCVFLSHGENDHVYAYDAQIKIETITNMFRGDKCQSLVGKPKIFIIQACRGDKH 180
                                                                                   TNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTEL
                                                                                                                                                                    SANEDSVDAKPDRSSFVPSLFSKKKKNYT-MRSIKTTRDRVPTYQYNNNFEKLGKCIIIN
                                                                                                          HEHFFWHLRLPDRRGTLADRNNLKRSLTDLGFEVRIFDD---LKAEDVLKKVFEASRDDY 120
                                                                                                                           NKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKK---ASEEDH
                                                                                                                                                    AAGRVQLDSKP----TPTTTADGNQNITEVDAFDKRRTFDPAEQYKMNHQRRGVALIFN 63
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                                                                                                                                                                                                                                                                                    ; PR00376; ILIBCENZYME. SM00115; CASC; 1.
                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                 Conservative
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                                           QADSGPINDT--DANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFV 242
                                                                                                                                                                                                           31.8%;
38.1%;
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21,
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                                                                                                                                                                                                          Score 512.5;
Pred. No. 9.
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51CE31EBCAAE7383 CRC64;
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Best Local
Q918S9;
01-OCT-2000 (
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01-MAR-2002 (
Caspase 6
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Pfam; PF00655; ICE_p20; 1.
Pfam; PF00656; ICE_p20; 1.
Pfam; PF00656; ICL_D20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1
PROSITE; PS01121; CASPASE_HIS; 1
PROSITE; PS01121; CASPASE_HIS; 1
PROSITE; PS0127; CASPASE_P10; 1
PROSITE; PS0127; CASPASE_P10; 1
PROSITE; PS50208; CASPASE_P20; 1
SEQUENCE 303 AA; 34132 MW; 4
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Q9IB66;
01-OCT-2000
                                                             Q918S9
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J. Biol. Chem. 275:1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=20209426; PubMed=10744739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
Amphibia; Batrachia; Anura; Mesobatra
                                                                                                                          247
                                                                                                                                                                       187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kenopodinae;
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                                                                                                                     KAYAASLEFTEILTLYNRKVSQRSVEYCNDPKAIGKKQIPCFASMLTKKLF
                                                                                                                                     EEHGKELEIMOILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELY 300
                                                                                                                                                                                          ---QADSGP---INDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSIL
                                                                                                                                                                                                                  FLCVFLSHGEDKHIYSYDSLIDIQELTNPFKGDKCKSLVGKPKIFILQACRGEKHDEPVL
                                                                                                                                                                                                                                                                                                                                      EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTR--DRVPTYQYNMNFEKLGKCIIINNK 76
                                                                                                                                                                    PKDEVDSVPLTNVTEVDAASLCTLPAGADFIMCYSVAEGYYSHRETVNGSWYIQDLCAVV
                                                                                                                                                                                                                                          FACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAI- 195
                                                                                                                                                                                                                                                                   DFYWQLRLGSRRGTNTDSMNLNRILTDLGFDVQNYYNLRTMDVLEKIQEASTTDHSNADC
                                                                                                                                                                                                                                                                                         NFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB038169;
                                                                                                                                                                                                                                                                                                                                                                              Similarity
             (TrEMBLrel.
                                    (TrEMBLrel.
                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
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             15,
15,
20,
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                                                                                                                                                                                                                                                                                                                  -EQKANVTETDGWTSRTVELDPSAEYIMTHKRRGLALIFNHE
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20,
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           Created)
Last sequence update)
Last annotation updat
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                              Score 510;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata;
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                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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n of .
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nes 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata;
                                                            B
                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
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           update)
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                                                                                                                                                                                                                                                                                                                                                                                          303;
                                                                                                                     297
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                                                                                                                                                                                          249
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 108
                                 Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebra: Mammalia; Eutheria; Cetartiodactyia; Ruminantia; Bovidae; Caprinae; Ovis.

RCBI_TaxID=9940;
                                                                                                      01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
            SEQUENCE FROM N.A.
                                                                                                Caspase-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                               077623;
                                                                                                                                                          077623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1999) to the EMBL; AF212219; AAF73848.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and sequencing mykiss, and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Actinopterygii, Neopterygii, Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; C14.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                   TRKLYF
                                                                                                                                                                                                                                          TKELYF 301
                                                                                                                                                                                                                                                               INGSWYIQDLCGAMRKFGDSLEFTELLTLVNRKVSMRSVGNCNDKTAIGKKQVPCFASML
                                                                                                                                                                                                                                                                                    GRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSML
                                                                                                                                                                                                                                                                                                                                   IQACRGTELDDAIQ----ADSG-PIND--TDANPRYKIPVEADFLFAYSTVPGYYSWRSP
                                                                                                                                                                                                                                                                                                                                                            ISQAAEANHADADCFVCVFLSHGENDHVYAYDDKIAIQDITALFKGDKCKSLVGKPKIFI
                                                                                                                                                                                                                                                                                                                                                                                  LKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFF
                                                                                                                                                                                                                                                                                                                                                                                                           NHKRRGLALIFNQEHFFWHLRMPPRNGTNADRSNLVKRFEDLNFEVQAFDNLKVEEVLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNM
                                                                                                                                                                                                                                                                                                              LQACRGDKHDDPVTPMDVVDSEVKTNEVVVDAGVVYTLPAGADFIMCYSVAEGYYSHRET
                                                                                                                                                                                                                                                                                                                                                                                                                                 NFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTKGSLEKDNKTSQTTGPSENLTETDGYFCSSSFSMD-------
  B.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P42574; 1PAU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS01122; CASPASE_CYS;
PS01121; CASPASE_HIS;
PS50207; CASPASE_P10;
PS50208; CASPASE_P20;
                                                                                             (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002398; ICE_p10.
IPR002138; ICE_p10.
IPR001309; ICE_p20.
 Hendry I.R.,
                                                                                                                                                                                                                    297
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                          08,
20,
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of caspa
its expr
Tilly J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
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f caspase 6 in
ts expression
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                                                                                                       Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.10); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 500.5; DB Pred. No. 1.1e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 1.
; 1.
; 1.
5A6B5F2BA0CFA660 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cunningham C., Secombes C.J.; 6 in rainbow trout, Oncorhynchus ion under conditions known to
 Hamernik D.L.;
                                                                                                                                                      182
                                                                      Vertebrata; Euteleostomi;
                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13;
                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125;
                                                           Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT
Q99M47
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  Query Match
Best Local Similarity
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Best Local
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                                                              PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JAN-2001)
EMBL; BC002022; AAHO
                                                                                                                                          PRINTS; PR00376; ILIBCENZYME SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001
01-JUN-2001
                                                                                                       PROSITE;
                                                                                                                              PROSITE;
                                                                                                                                                                                                     Pfam; PF00655; ICE_p10; 1. Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                      MGD; MGI:1312921;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CASP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q99M47;
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                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01122; CASPASE_CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002138; InterPro; IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; C14.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P42574; 1PAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF068837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Accumulation of Caspase-3 mRNA and Induction of Caspase Activity the Ovine Corpus Luteum Following Prostaglandin-F2a Treatment In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LELMSDVSKEDHSKRSSFICVLLSHGEEGIIFGTNGPVDLKKLASFFRGDCCRSLTGKPK
                                                                                                                                                                                                                                                                                                                             P42574; 1PAU
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                                                          3; PS01122; CASPASE_CYS;

3; PS01121; CASPASE_H1S;

3; PS50207; CASPASE_P10;

3; PS50208; CASPASE_P20;

3; PS50208; CASPASE_P20;

4; PS50208; CASPASE_P30;

5; PS50208; CASPASE_P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; PR00376; IL1BC
SM00115; CASC;
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: IPR002138;
: IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              AAH02022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998) to the AAC25713.1;
                                                                                                                                                                                                                                                                                                    Casp6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                          ICE_p10.
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  30.0%;
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2.1;
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17,
20,
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Last sequence upo
Last annotation
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Score
Pred.
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Pred. No. 2.6e
30; Mismatches
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                                                   ; 1.
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5965C5932A127B6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B5860C6996C21BE7 CRC64;
  483.5; DB 11;
No. 3.6e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O35397;
O35397;
O1-JAN-1998
O1-NOV-1998
O1-MAR-2002
Caspase 6.
                                                                                                                                                                                                                                              PROSITE; PS01122; CASPASE CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF025670; AAC25433.1; -. HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY Kaushal G.P., Singh A.B., Shah S.V.; "Rat kidney Mch2.";
                                                                                                                                                                                                                                                                                                          PRINTS; PR00376; IL1BCENZYME. SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                      Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Rokarvota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; C14.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
136 GKPKIFIIQACRGSQHDVPLVPLDVVDHQTDKLDDNVTQVDAASVYTLPAGADFLMCYSV
                                  176
                                                                                           116
                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                     [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                 [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 QVPCFASMLTKKLHF 270
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                                                              76
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                                                                                                                                                                                         Local
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                          EKPKLFFIQACRGTELD-----DAIQADSGPIND----TDANPRYKIPVEADFLFAYST
                                                                                  CAKMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLL 175
                                                                                                                PAEQYKMDHKRRGTALIFNHERFFWHLALPERRGTNADRDNPTRRFSELGFEVKCFNDLR 75
                                                                                                                                         PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS 115
                                                       AEELLLKIHEVSTSSHVDADCFLCVFLSHGEGNHIYAYDAKIEIQTLTGLFKGDKCQSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QIPCVVSMLTKELYF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKPKIFIIQACRGSQHDVPVVPLDVVDHQTDKLDNVTQVDAASVYTLPAGADFLMCYSVA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEELLLKIHEVSTSSHIDADCFICVFLSHGEGNHVYAYDAKIEIQTLTGLFKGDKCQSLV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAKMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGYYSHRETVNGSWYIQDLCEMLARYGSSLEFTELLTLVNRKVSQRRVDFCKDPDAIGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKPKLFFIQACRGTELD------DAI--QADS-GPINDTDANPRYKIPVEADFLFAYSTV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAEQYKMDHKRRGVALIFNHERFFWHLTLPERRGTNADRDNLTRRFSDLGFEVKCFNDLR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100; Conservative
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                IPR002138; ICE_p10.
IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                  IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 05,
(TrEMBLrel. 08,
(TrEMBLrel. 20,
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                   31556 MW;
                                                                                                                                                                         29.8%; Score 481; DB 11; 38.7%; Pred. No. 6.2e-36; tive 43; Mismatches 104,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                  69D999E729B3BDE2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
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                                                                                                                                                                          104;
                                                                                                                                                                                                     Length
                                                                                                                                                                          Indels
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Q9BQE7
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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                  Protease.
SEQUENCE
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Q9BQE7;
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01122; CASPASE_CYS;
PROSITE; PS01121; CASPASE_HIS;
PROSITE: PS50207; CASPASE_P10;
PROSITE: PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00655; ICE_p10; I.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL; BC004460; AAH04460.1; -. EMBL; BC000305; AAH00305.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10
InterPro; IPR001309; ICE_p20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; C14.005;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 273
                                                              213
                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FISSUE-LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 VPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEK
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             KQIPCVVSMLTKELYF
KOVPCFASMLTKKLHF
                                                         AEGYYSHRETVNGSWYIQDLCEMLGKYGSSLEFTELLTLVNRKVSQRRVDFCKDPSAIGK
                                                                                  VPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEK
                                                                                                                    GKPKIFIIQACRGNQHDVPVIPLDVVDNQTEKLDTNITEVDAASVYTLPAGADFLMCYSV
                                                                                                                                                  EKPKLFFIQACRGTE-----LDDAIQADSGPINDTDANPRYKIPVEADFLFAYST 225
                                                                                                                                                                                   AEELLLKIHEVSTVSHADADCFVCVFLSHGEGNHIYAYDAKIEIQTLTGLFKGDKCHSLV
                                                                                                                                                                                                                CAKMODLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLL 175
                                                                                                                                                                                                                                                PAEKYKMDHRRRGIALIFNHERFFWHLTLPERRGTCADRDNLTRRFSDLGFEVKCFNDLK 92
                                                                                                                                                                                                                                                                               PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQIPCVVSMLTKELYF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEGYYSHRETVNGSWYIQDLSEMLARHGSSLEFTELLTLVNRKVSQRRVDFCKDPGAIGK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KQVPCFASMLTKKLHF 271
                                                                                                                                                                                                                                                                                                                   l Similarity
98; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                293 AA;
                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                33310 MW;
                                                                                                                                                                                                                                                                                                                               29.4%; Score 474; DB 4; 38.3%; Pred. No. 2.9e-35;
                           301
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                0738AE4F9791EBD7 CRC64;
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                                                                                                                                                                                                                                                                                                                 Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293
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                                                                                                                                                                                                                                                                                                                                             Length 293;
                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                            Gaps
                                                                                       285
                                                                                                                                                                                                                                                                               115
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Search completed: December 2, 2002, 12:58:10 Job time: 29.7328 secs

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Minimum
Maximum
                                                                                                                                                                                                                                              Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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DB
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        A_Geneseq_101002:*
1: /SIDS2/qcadata/
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Gapop 10.0 , Gapext 0.5
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//SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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      AAW15247
AAW15262
AAY2160604
ABJ01222
ABB09297
ABB09299
ABB09399
ABB09300
ABB78588
                                                                                                                                                                                                                                                                                   SUMMARIES
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                                                                                                                                                                                                                     Description
                                                                                                                                                          Cysteine protease
Apototic protease
                                                                                                    Human
                                           Human
                                                               Human
                                                                                                                           Human
                                                                                                                                         Amino
                                                                                  Human
                                                                                                                                                                                                                                                                                                                                      being printed,
o acid sequenc n caspase-7. SE n caspase 7 pr n caspase 7 pr n caspase 7 pr n caspase 7 pr n interleukin-e caspase 7 pr
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se 8	AAE06523	22	480	•	447.5
оѓур	AAW54392	19	389	27.8	449
caspase	AA021925	23	293	•	466
casp	AAE00603	22	293	•	466
yste	AAW06244	18	293	•	466
leukin 1 c	AAY85062	21	401	•	468
leukin 1 con	AAY85061	21	278	•	468
caspase-6	ABJ01221	23	293	•	474
o acid seque	AAY21720	20	293	•	474
e caspase	AA021924	23	276	•	483.5
ophila melano	ABB61468	22	323	٠	$\frac{\omega}{2}$
osophila me	ABB58379	22	339		539
rtate-speci	AAW89198	20	299	•	552
e caspase 3	AAU05395	22	277	•	703
pase-3	AAB59579	22	245	٠	706
⋾	AAE00610	22	261		707
leuk	AAW47089	19	277		709
human	AAW48937	19	277		. 711
man	AAW48945	19	277		711
e-3. Unid	AAB98654	22	241		716.5
	ABJ01218	23	277		718
caspase-3	AAE00600	22	277	4.	718
caspa	AAU05394	22	277	44.5	718
acid sequ	AAY21717	20	277	4	718
n CPP32a pr	AAW16600	17	277		718
an casp	AAB26763	21	249		719.5
Pig caspase #2. S	AAG78712	22	277	4.	2
acid	AAW41688	19	277	4	721
n interleukin	AAR95831	17	277	4.	721
a. Homo	AAW00677	17	277	4.	721
n CPP32beta	AAW00372	17	277	٠.	721
pase 7	ABB78587	23	253	œ	8
ine protease	AAW15263	18	253	48.6	783.5
ase-7. Unide	AAB98655	22	244	0	1.1
Mouse caspase 7 pr	АВВ09298		4		1.4

ALIGNMENTS

RESULT 1 AAW15247

AAW15247 standard; Protein; 303 AA

Cysteine protease CMH-1.

21-JUL-1997 AAW15247;

(first entry)

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Cysteine protease; CMH-1; CPP32/Mch2 homologue-1; apoptos programmed cell death; cancer; neurodegenerative disease; autoimmune disease; gene therapy; diagnosis.
09-MAY-1997
                 W09716552-A1
                                           Active-site
                                                                                        Protein
                                                                                                                                             Key
                                                            Active-site
                                                                                                                  Protein
                                                                                                                                    Peptide
                                                                                                                                                               Homo sapiens
                                                            /note=
155
                                                                                      /label= Mat_protein
/note= "active CMH-1
29..303
                                           /note= "Hisl44 is a catalytic residue"
186
                                   /note= "Cys186 is a catalytic residue"
                                                                                                                                            Location/Qualifiers
                                                                                                                          /label= Pro-peptide
                                                                                'label=
                                                                      "active CMH-1
                                                                              Mat_protein
                                                                    polypeptide (Claim
                                                                                               polypeptide (Claim 3)"
                                                                                                                                                                                                 apoptosis;
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AAW15262
ID AAW1
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AC AAW1
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Best Local S
Matches 301
Mch3-alpha; cysteine protease;
neurodegenerative disease; the;
                                                                   Apototic protease Mch3-alpha.
                                                                                                                   05-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated CDNA clone (AAT66970). Active, activatable (i.e. proenzyme) or inactivated forms of CMH-1 can be expressed in prokaryotic or eukaryotic host cells. The polypeptides are useful for screening potential apoptosis inhibitors and for raising antibodies used to assay CMH-1, to regulate cholesterol levels, inhibit CMH-1 activity and therefore apoptosis, and to purify CMH-1 polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-1995;
03-NOV-1995;
06-NOV-1995;
                                                                                                                                                                AAW15262
                                                                                                                                                                                                         AAW15262 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A proenzyme (AAW15247) is activated to CMH-1, or CPp32/Mch2 homologue-1, a human cysteine protease that is involved in apoptosis. Its amino acid sequence was deduced from a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding active, activatable or inactive cysteine - useful in gene therapy for promoting and inhibiting for diagnosing cells with potential for apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lippke JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proenzyme (AAW15247) is activated
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                                                                                                                                                                                                                                                                                                                                                                                                                          FVQALCSILEEHGKELEIMQILTRVNDRVARHFESOSDDPHFHEKKQIPCVVSMLTKELY
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                                                                                                                                                                                                                                                                                                                                                              FSQ 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY 60
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DB; AAT66970.
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                                                                                                                                                                                                                                                                                                                      303
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                                                                                                             (first entry)
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95US-0007211.
95US-0007251.
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                                                                                                                                                                                                     Protein;
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99.3%;
therapy; diagnosis.
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Pred. No. 1
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1.4e-161;
                    ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Query Match 99.0
Best Local Similarity 99.3
Matches 301; Conservative
                                                                                                                                                                                                                                                  Human Mch3-alpha (AAW15262) is an apoptotic protein and novel member of the interleukin-1-beta converting enzyme (ICE) family of cysteine proteases. Its amino acid sequence was deduced from a cDNA clone (AAT66992) obtd. from a Jurkat library. Mch3-beta (AAW15263) has also been identified that lacks the active site of Mch3-alpha. Mch3-alpha polypeptides can be produced in engineered host cells and used to treat human diseases associated with cell death, such as AIDS, ischaemic injury, neurodegenerative diseases, etc. They can also be used to regulate apoptosis and to screen for Mch3-alpha polypeptides.
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                             New gene encoding Mch3, a cysteine protease that regulates - for treating human diseases associated with apoptosis, an screening for antagonists and agonists of Mch3
                                                                                                                                                                                                                                               agonists
                                                                                                                                                                                                                                                                                                                                                                           Claim
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Tomaselli K;
                181
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FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
                                             DLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKL
                                                                                                                                        MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY
                                  DLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKL
                                                                                            NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ
                                                                                                                            NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ
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                                                                                                                                                                                                                                               and antagonists.
                                                                                                                                                                                                                        303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHARM INC.
JEFFERSON THOMAS
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184..188
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199..30
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Pred. No. 1.4e
1; Mismatches
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                                                                                                                                                                                   DB 18;
1.4e-161;
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                                                                                                                                                                                                                                                                                                                                                                                                          es apoptosis
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RESULT 3
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                                                     Query Match
Best Local S
Matches 301
                                                                                                                                                                                                                 Rev-caspases are cysteine proteases that specifically cleave proteins after Asp residues and is expressed as a zymogen, in which the small subunit is N-terminal to a large subunit. A gene delivery vehicle comprising a rev-caspase coding sequence is useful for the treatment of cancer, where the gene delivery vehicle is internalised by tumour cells. The gene delivery vehicle is internalised by tumour cells transfected with a rev-caspase expressing vector can be used in identification of inhibitors or enhancers of caspase mediated apoptosis.
                                                                                                           Sequence
                                                                                                                                      gene
                                                                                                                                                enhancer of caspase processing activity. Caspase inhibitors are useful for treating neurodegenerative diseases as well as for inhibiting apoptosis in the heart following myocardial infarction. Sequences AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10
                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 17A-B;
                                                                                                                                                                                                                                                                                                                                                                                         cancer
                                                                                                                                                                                                                                                                                                                                                                                                                    New
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rev-caspase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of caspase-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY21721;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-1999
                                                                                                                                                                                                       In vitro translated rev-caspase can be used to identify an inhibitor
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            1 MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY 60
                                                                                                                                                                                                                                                                                                                                                                                       isolated nucleic acid molecule encoding a rev-caspase - used screening and identifying inhibitors or enhancers for treating cer or autoimmune disease
                                                                                                                                                                                                                                                                                                                               invention relates to nucleic acid molecules encoding rev-caspases
                                                                                                                                                                                                                                                                                                                                                                                                                                               1999-419353/35
DB; AAX81223.
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                                                                                                                                     products (AAY21715-Y21724).
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cysteine protease; zymogen; caspase; cancer; gene therapy; isease; caspase-mediated apoptosis; neurodegenerative; myocardial infarction; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JEFFERSON THOMAS
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                                                                99.6%;
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RESULT 4
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                                                                          Novel fusion polypeptide comprising first and second caspase subunit separated by cleavage site not associated in nature with caspase subunit, useful for cloning gene encoding enzymes involved in
                                                                                                                                                                                                                                                                                                                                                                                 Human; caspase-7; interleukin-1 converting enzyme; ICE-LAP3; CHM-1; Micysteine protease; apoptosis; caspase expression cassette; metastasis; tumour; cathepsin B; urokinase; proliferation; gene therapy.
                                               Claim
                                                                                                                                                Cordell B,
                                                                                                                                                                                                                                                                                          Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE00604 standard; Protein; 303 AA
                                                                  proteolytic cleavage
                                                                                                                    N-PSDB;
                                                                                                                                                                                                   20-OCT-1999;
                                                                                                                                                                                                                      19-OCT-2000; 2000WO-US28941
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                                                                                                                                                                                                                                                                                                              Cleavage-site
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                                                                                                                                                                    (SCIO-) SCIOS INC
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DB; AAD03914.
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                                                                                                                                                  Li Y;
                                               14; 116pp;
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                                                                                                                                                                                                   99US-0160559
                                                                                                                                                                                                                                                                                           206.
                                                                                                                                                                                                                                                                                                               /label= Proteolytic_cleavage_site 198..199
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23..24
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                                                                                                                                                                                                                                                                                 /label= Proteolytic_cleavage_site
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                                              English
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The present amino acid sequence is human Caspase-7 also known as interleukin-1 converting enzyme (ICE) LAP3, CHM-1 and Mhc3. Caspases a family of cysteine proteases, that participate in the initiation and

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Caspases

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RESULT 5
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding two caspase subunits. A fusion polypeptide comprising a first and a second caspase subunit, separated by a cleavage site not associated in nature, is useful for cloning gene encoding enzymes involved in proteolytic cleavage. An expression cassette containing fusion polypeptide is used to identify a mutant cell line deficient in an enzyme of interest and is also useful for diagnosis and suppression of proliferation or metastases of a tumour cell characterised by overexpression of a polypeptide (e.g. Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA encoding fusion polypeptide is used in gene therapy.
                       09-JAN-1998;
62-JAN-1999;
                                                                                                                                                                                                                                                               ABJ01222 standard;
                                                                                                        US6376226-B1
                                                                                                                                                        cancer;
                                                                                                                                                                                                                  18-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cleavage into a large and small subunit, occurring after specific aspartic acid residues within the pro-enzyme sequence. The present invention relates to a method for functional cloning of genes encoding proteins or enzymes involved in proteolytic cleavage. The invention is based on the use of caspase expression cassettes comprising the coding sequence of a proteolytic cleavage site flanked by sequences
                                                         26-APR-2000;
                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                         caspase-7
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 VIND
                                                                                                                                                       autoimmune
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JEFFERSON THOMAS
                                                        2000US-0561756
                                                                                                                                                                                                                (first entry)
                      98US-070897P.
99US-0227721.
                                                                                                                                                                 rev-caspase;
                                                                                                                                                                                        SEQ
                                                                                                                                                       disease;
                                                                                                                                                                                                                                                                 Protein; 303
                                                                                                                                                                                        ID NO:
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99.3%;
                                                                                                                                                                                        24
                                                                                                                                                    ; gene therapy; protease; apoptosis;
cytostatic; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1606; D
Pred. No. 1.4e
1; Mismatches
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                                                                                                                                                   immunosuppressive
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1.4e-161;
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RESULT 6
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Best Local Similarity
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                                                                                                                    Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition hyperproliferative disorder; cancer; bone metabolism; infectio cholesterol disorder; inflammation; tumour.
                                               21-MAR-2002
                                                                     WO200222640-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of human rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences can be used in the gene therapy of cancer and autoimmune diseases. The present sequence is a protein described in the exemplification of the
                     10-SEP-2001; 2001WO-US28232
                                                                                            Homo sapiens
                                                                                                                                                                              Human caspase 7 protein sequence
                                                                                                                                                                                                          15-JUL-2002
                                                                                                                                                                                                                                                          ABB09297 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Pred. No. 1.4e-161;
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Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition hyperproliferative disorder; cancer; bone metabolism; infection
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                                                         7 protein sequence SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a human caspase 7 example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antisense compounds targeted to nucleic acids encoding caspase for modulating gene expression and treating diseases associated with expression of caspase 7 in humans \,
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antisense compounds targeted for modulating gene expression and expression of caspase 7 in humans
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              FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240
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                                                                                                                                                                                                                                                                                                               the present invention.
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                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                              This ICE-LAP-3 protein may be used therapeutically,
                                                                                                                                                                                                                                                                                                                  Claim 1; Page 91-92; 67pp; English.
                                                                                                                                                                                                                                        therapy applications.
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                                                                                                                                                  ഗ
                                                                                                                                     QGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSQ
                                             KASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQ
                                                                                        EKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLK 124
                                                                                                                         QGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNF 139
                                KASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQ
                                                                             EKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -3; interleukin-I-converting
Alzheimer's disease; Parkins
                                                                                                                                                                                                                                                                                                                                                                                                                        GA,
                                                                                                                                                                                                                                                    cells for cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
                                                                                                                                                                                                                                                  or antiviral agent and to control embryonic developm e homeostasis. The protein can also be used to treat pression disorders, such as AIDS, by targeting virus cells for cell death. The DNA may find use in gene
                                                                                                                                                                                                                  341 AA;
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                       He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0334251
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                                                                                                                                                                                                                                                                                                                                                                                                                       Σ
                                                                                                                                                                                 84.7%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Hudson PL,
                                                                                                                                                                     Score 1366; D
Pred. No. 4.7e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme-like
                                                                                                                                                                     DB 17;
1.7e-136;
nes 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis
                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease-3.
                                                                                                                                                                                                                                                                                 .g. as an
development
                                                                                                                                                                                                                                                                        to treat
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                                                                                                                                                                      Gaps
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RESULT 10
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                                                                                                                                                                                                                          The present invention describes a compound (I) 8-50 nucleobases in clearly hargeted to a nucleic acid molecule encoding caspase 7, which specifically hybridises with and inhibits the expression of caspase 7. (I) has antiinflammatory and cytostatic activities, and can be used in antisense therapy and as an inhibitor of caspase 7 expression. (I) is useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition associated with caspase 7 including inflammatory condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (I) is useful prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence represents a mouse caspase 7 protein, which is used in an example from the present invention.
                                                                                                                                              Query Match
Best Local
                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antisense compounds targeted to nucleic acids encoding caspase for modulating gene expression and treating diseases associated with expression of caspase 7 in humans \cdot
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-401902/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cholesterol disorder; inflammation; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition; hyperproliferative disorder; cancer; bone metabolism; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse caspase 7 protein sequence SEQ ID NO:97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB78588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB78588 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320
     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260
                                 61
                                                                                                                                              Local Similarity
                    NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ 120
                                                                                MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY
RMDFQKMGKCIIINNKNFDKATGMDVRNGTDKDAGALFKCFQNLGFEVTVHNDCSCAKMQ
                                                              MTDDQDCAAELEKVDSSSEDGVDAKPDRSSIISSILLKKKRNASAGPVRTGRDRVPTYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCSILEEHGKDLEIMQIL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACRGTELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN80919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watt AT;
                                                                                                                                                                                               303
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 121-123; 138pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US28232
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                                                                                                                                              83.4%;
81.5%;
                                                                                                                               27; Mismatches
                                                                                                                                            Score 1346; DB 23;
Pred. No. 5.2e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                             Indels
                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                  The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding caspase 7, which specifically hybridises with and inhibits the expression of caspase 7.

(I) has antiinflammatory and cytostatic activities, and can be used in antisense therapy and as an inhibitor of caspase 7 expression. (I) is useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition associated with caspase 7 including inflammatory condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (I) is useful prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence represents a mouse caspase 7 protein, which is used in an example from the present invention.
                          example
                                                                                                                                                                                                                                                                     Novel antisense compounds targeted for modulating gene expression and expression of caspase 7 in humans
                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                         Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense therapy; caspase 7 inhibitor; inflammatory hyperproliferative disorder; cancer; bone metabolism;
                                                                                                                                                                                                                                           Example 13; Page 97-99; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-2000; 2000US-0659860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cholesterol disorder; inflammation; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse caspase 7 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB09298 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-2001; 2001WO-US28232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2002 (first entry)
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DB; ABN80832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFIQACRGTELDDGIQADSGPINDIDANPRNKIPVEADFLFAYSTVPGYYSWRNPGKGSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
                                                                                                                                                                                                                                                                                                                                                                                                     ISIS PHARM INC
                         from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; antisense modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303
                                                                                                                                                                                                                                                                                                                                                                         Watt AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                        to nucleic acids encoding caspase treating diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
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                                          The present invention relates to a molecule or molecular complex (I) comprising a binding pocket defined by the structure coordinates of caspase-7 amino acids 234, 235, 237, 276, 278, 281, and 284 or a homolo of (I) with a binding pocket having a root mean square deviation from t amino acid backbone atoms of not more than 1.5 Angstrom, where (I) has $4 binding region that is more hydrophilic than that of caspase-3. The present sequence is caspase-7, which was used in a sequence homology
                                                                                                                                                                                                                                                                                              Molecule or molecular complex used for drug discovery, comprises a binding pocket of caspase-7 or a homolog having an S4 binding region more hydrophilic than that of caspase-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caspase-1; caspase-3.
                                                                                                                                                                                                                                                      Example 4; Fig 3;
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-329229/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
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247; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US31602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                   161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           co-ordinate
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81.5%;
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Pred. No. 6.2e-134;
27; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         data; caspase-7; S4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                homolog from the
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RESULT 13
AAW15263
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Best Local S
Matches 242
                                   New gene encoding Mch3, a cyst for treating human diseases
                       Claim
                                                                       WPI; 1997-289289/26
N-PSDB; AAT66993.
                                                                                               Alnemri ES,
Tomaselli K;
                                                                                                                       (IDUN-) IDUN
                                                                                                                                               13-NOV-1995;
                                                                                                                                                               12-NOV-1996;
                                                                                                                                                                                22-MAY-1997.
                                                                                                                                                                                               WO9718313-A1
                                                                                                                                                                                                                       Cleavage-site
                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                               Mch3-beta; cysteine protease; apoptosis; AIDS; neurodegenerative disease; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                        Cysteine protease Mch3-beta
                                                                                                                                                                                                                                                                                                                         05-AUG-1997
                                                                                                                                                                                                                                                                                                                                                          AAW15263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFSQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                 YFSQ 303
                                                                                                                                                                                                                                                                                                                                                                                                                                         WFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                 WFVQALCSILEEHGKDLEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKEL
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242; Conser
                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
                       1:
                                                                                                      Armstrong
                                                                                                                       JEFFERSON THOMAS
                                                                                                                               PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                               96WO-US18118
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                                                                                                                                                                                                                        /label
                                                                                                                                                                                                                                        Location/Qualifiers 24..28
                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.8%;
99.2%;
                      English.
                                                                                                                                                                                                                                l= P20
                                                                                                     ৾ৢ≂
                                     a cysteine protease that regulates apoptosis seases associated with apoptosis, and ts and agonists of Mch3
                                                                                                                                                                                                                P17
                                                                                                       Fernandes-Alnemri
                                                                                                                                                                                                                                                                                                                                                          253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1304; DB 22;
Pred. No. 1.1e-129;
l; Mismatches 1;
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                                                                                                                                                                                                                                                                                         ischaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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Human Mch3-beta

converting

(AAW15263) is a novel member of enzyme (ICE) family of cysteine

the interleukin-1-proteases. Its

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RESULT 14
ABB78587
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 148;
The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding caspase 7, which specifically hybridises with and inhibits the expression of caspase 7 (I) has antiinflammatory and cytostatic activities, and can be used:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition; hyperproliterative disorder; cancer; bone metabolism; infection; cholesterol disorder; inflammation; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not include the QACRG active site pentapeptide sequence of Mch3-alpha. Mch3-beta polypeptides can be produced in engineered host cells. They can be used as dominant/negative inhibitors of apoptotic Mch3-alpha to treat or reduce the severity of diseases characterised by increased programmed cell death, such as AIDS, ischammic injury, neurodegenerative diseases, etc., and can also
                                                                                                                                                                                                                                                                                                                                                                                                           W0200222640-A1
                                                                                                                                                                                                                                                                                                      11-SEP-2000; 2000US-0659860
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human caspase 7 protein sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from a Jurkat library. Mch3-beta mRNA arises from 2 simultaneou alternative splicing events that result in a shift in the reading frame after amino acid 148 of Mch3-alpha (AAW15262). Mch3-beta d
                                                                                                                                                                                                                                                                                                                                       10-SEP-2001; 2001WO-US28232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB78587 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid sequence was deduced from a cDNA clone (AAT66993) obtd. from a Jurkat library. Mch3-beta mRNA arises from 2 simultaneous
                                                                                 Example 15;
                                                                                                                    expression
                                                                                                                                Novel antisense compounds targeted to nucleic acids encoding caspase 7, for modulating gene expression and treating diseases associated with
                                                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                  modulating gene expression and ression of caspase 7 in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLLKKASEEDHTNAACFACILLSHGEENV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ 120
                                                                                                                                                                                     2002-401902/43.
DB; ABN80841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLLKKASEEDHTNAACFACILLSHGEENM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                      Watt AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253
                                                                                 Page 105-107; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for Mch3 agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9e-74;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition associated with caspase 7 including inflammatory condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (1) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (1) is useful prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence represents a human caspase 7 protein, which is used in an
                                                                                                                                                                                                                                                                                                                                  pro-inflammatory; pro-apoptotic; apoptosis; inflammation; anti-
antisense DNA; treatment; immunne; proliferation; degeneration;
disease; AIDS; acquired immunodeficiency syndrome; autoimmune;
pathogenic infection; cardiovascular; neurological; injury;
alopecia; ageing; cancer; type I diabetes; Parkinson's;
                                                                                                                                                                                                                                                                                                                                                                                                     CPP23beta; isoform; inactive; CPP32; proenzyme; cysteine; protea proteolytic product; poly(DP-ribose) polymerase; PARP; apopain; cleavage enzyme; human; monocytic leukaemia; cell line; THP-1; identification; modulator; recombinant production; gene therapy;
                                       Protein
                                                                              Region
                                                                                                                       Region
                                                                                                                                      Cleavage-site
                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW00372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                   Protein
                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                         Alzheimer's.
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                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLLKKASEEDHTNAACFACILLSHGEENM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity
148; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                        /note= "1
175..176
176..193
                                                                                                                                                                                                          /note=
28..29
29..46
                                     176..277
                                                                                161..165
                                                                                                                                                                   29..175
                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.6%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as an inhibitor
                        "12 kDa subunit p12'
                                                                                                          "amino-terminal sequence
                                                                                                                                                                                                                                      "amino-terminal pro-domain"
                                                                                                                                                                                             "amino-terminal sequence determined
                                                   "conserved pentapeptide containing catalytic cysteine"
                                                                                           purified
                                                                                                                                                                             purified
                                                                                                                                                 kDa subunit p17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 783.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                              enzyme
                                                                                           enzyme
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Best Local Similarity
Matches 144; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown function cloned from Jurkat cells), the proteolytic product of which is the poly(DP-ribose) polymerase (PARP) protease, apopain. The PARP cleavage enzyme was purified from the human monocytic leukaemia cell line, THP-1, using standard ion exchange chromatography techniques and SDS PAGE. Apopain can be used to identify apopain activity modulators, while apopain encoding DNA may be used for apopain production or in gene therapy (i.e. in vivo or ex vivo gene transplantation) for enhancing the pro-inflammatory or pro-apoptotic effects of apopain. Anti-apopain antibodies and antisense DNA can be used to reduce or eliminate the pro-inflammatory or pro-apoptotic effects of apopain. Modulation of apopain activity is beneficial in the treatment of immune,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the CPP23beta or Glu190 isoform of the inactive CPP32 proenzyme (a member of the interleukin converting enzyme/pro-apoptotic protein CED-3 family of cysteine proteases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apopain, a new human apoptosis related enzyme - responsible for the proteolytic breakdown of poly(ADP- ribose) polymerase (PARP) which occurs at the onset of apoptosis
                                                                                                                                           and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferative and degenerative diseases, e.g. AIDS, autoimmune disease, pathogenic infections, cardiovascular and neurological injury, alopecia, ageing, cancer, type I diabetes and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 4C; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-485775/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC.

(MERI ) MERCK FROSST CANADA INC.
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                                  259 MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
                                                                                                                                                                                                                    56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
                                                                                                                                                                                                                                           79 DKYTGMGYRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                               19 EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTVQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                                                                                    S
                                                                                           SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEI 258
MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                      SGVDDDMAC----HKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEF 232
                                                                                                                                                                                                                                                                                              ENSYDSKSIK-NLEPKIIHGSESMDSGISLDNS:----YKMDYPEMGLCIIINNKNF 55
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Search completed: December 2, Job time : 34.9569 secs

2002, 12:56:03

time : 34.9569 secs

Sequence 40, Appl Sequence 35, Appl Sequence 36, Appl Sequence 24, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 18, Appl Sequence 9, Appli

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Maximum DB seq
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Copyright (c) 1993 - 2002 Compuç
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10 US-09-954-697-2
10 US-09-955-697-12
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10 US-09-954-697-3
10 US-09-954-697-3
10 US-09-954-697-3
10 US-09-954-697-3
10 US-09-954-697-3
10 US-09-952-768-2
10 US-09-952-768-2
10 US-09-862-915-1
10 US-09-952-697-2
10 US-09-954-697-2
10 US-09-954-697-3
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  Sequence 2, Appli
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Sequence 34, Appli
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US-09-895-263-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09895263
Patent No. US20020076793A1
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
APPLICANT: He, Wei-Wu et al.
Like Apoptosis Protease 3 and 4
                                                                          INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/895,263
FILING DATE: 02-Vu1-2001
CLASSIFICATION: <UNBER: US/09/895,263
FILING DATE: 02-Vu1-2001
CLASSIFICATION: <UNBER: US/09/895,263
                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-251-6015
TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Ave.
  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357.5

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                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 41,119
                                                                                                                                                                                                                                                                                                                       NAME: Jonathan L. Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville
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10 US-09-954-697-30

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10 US-09-988-243-2

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10 US-09-988-243-2

10 US-09-988-243-2

10 US-09-989-903-40

10 US-09-989-903-24

10 US-09-9845-028-9

10 US-09-985-033-2

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10 US-09-985-033-3

US-09-985-033-9
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Sequence 1, Appli
Sequence 30, Appli
Sequence 20, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 48728, A
Sequence 9, Appli
Sequence 28, Appli
Sequence 47950, A
Sequence 47950, A
Sequence 47950, A
Sequence 35, Appl
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Best Local 9
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LENGTH: 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/09561756
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Albemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/227,721
PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEO ID. NOS: 116
                                                                                                                                                                                                                                                                                                     LENGTH: 30
TYPE: PRT
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                                  FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240
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                                                                            FFIQACRGTELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
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Pred. No. 6.4e-174;
1; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND TITLE OF INVENTION: THEREOF FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                         RESULT 4
US-08-556-627A-2
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; ORGANISM: Homo
US-09-227-721-24
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Best Local Similarity
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Patent No. 6379950
                                                                                                                                   APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: Mucleic Acids
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell and Flores
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Alnemr
                                                                                                                                                                                                    APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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COUNTRY:
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CITY: San Diego
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nilarity 99.3%;
Conservative
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Pred. No. 6.4e-174;
1; Mismatches 1;
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Acids Encoding
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Matches
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Patent No. US20020076793A1
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
Like Apoptosis Protease 3 and 4
                                                                                                                                                                                                                                                                                                Query Match
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INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                        19 EDSVDAKPDRSSFVPSLFSKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
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                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 301-251-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Some Street: 9410 Key West Ave
                                                                                                        NUMBER OF SEQUENCES:
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                                    CVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETD
                                                             CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEI
                                                                                                                                             DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                 ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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RESULT 6
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US-10-103-448-3
                                                                        SEQ ID NO 3
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Patent No. US20020155579A1
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                                                                                                                                                                   APPLICANT: Wu, Joseph C.
TITLE OF INVENTION: COMPRISING THE SAME AND ME
FILE REFERENCE: 480140.468D1
                                                                                                                                                                                                                               APPLICANT: Krebs, Joseph F.
APPLICANT: Srinivasan, Anu
APPLICANT: Fritz, Lawrence
APPLICANT: Wu, Joseph C.
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TITLE OF INVENTION: RECOMBLUANT, ACTIVE CASPASES
TITLE OF INVENTION: THEREOF
                                                                                          NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ for
                                                                                                                               CURRENT APPLICATION NUMBER: US/10/103,448
CURRENT FILING DATE: 2002-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-09-14
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                                  LENGTH: 264
TYPE: PRT
                ORGANISM: Homo sapien
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Best Local Similarity
TELEFAX: 30
INFORMATTION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                              TELEPHONE: 301-309-8504
                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                               FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: He, Wei-Wu et al. TITLE OF INVENTION: Interleu TITLE OF INVENTION: Like Apo
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CTTY: Rockville
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                                                               REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF140P1
                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 05-JU
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STRANDEDNESS: si
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                                                                                               Brookes, A. Anders
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9410 Key
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05-JUN-1995
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                                  Patent No.
                                                Sequence 6,
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Best Local Similarity
Matches 144; Conserv
                  GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 277 amino acids
                                                                                                                                                    259 MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
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                                  6114132 08/08964313
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DESMARAIS, SYLVIE
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linear
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; Pred. No. 1.6e-73;
50; Mismatches 77;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03-NOV-1996 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version
CURRENT APPLICATION DATA: NUMBER OF SOCIETY OF S APPLICANT: FORD-HUTCHINSON, ANTHONY
TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
NUMBER OF SEQUENCES: 15 APPLICANT: FILING DATE: 03 -NOV-199 ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette APPLICANT: APPLICANT: APPLICANT: APPLICATION NUMBER: FILING DATE: 04-NO REFERENCE/DOCKET NUMBER: 19824Y NAME: DURETTE, PHILIPPE L. REGISTRATION NUMBER: 35,125 CLASSIFICATION: COUNTRY: 07065 RAHWAY Ŋ USA SKOREY, KATHRYN NICHOLSON, DONALD RAMACHANDRAN, CHI FRIESEN, RICHARD GRESSER, MICHAEL FRIESEN, KENNEDY, 04-NOV-1997 BRIAN US/08/964,313 CHIDAMBARAN

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FILE REFERENCE: 480140.431D2
CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapien
US-09-954-697-33
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Best Local Similarity
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                                        PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
                                                                                                                              CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
                                                                                                                                                                                                                                                                                                       APPLICANT:
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                  APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
                        NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 VFQWLGFTVHIHNNVTKVEMEMVLQKQKCNPAHADGDCFVFCILTHGRFGAVYSSDEALI 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 IEEQGVEDSANEDSVDAKPDR-SSFVPSL-------
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Schneider, Pascal
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Hahne, Michael
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Burns, Kimberly
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Steiner, Veronique
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33.5%;
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Pred. No. 1.5e-37;
B; Mismatches 109;
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; ORGANISM: Homo sapiens US-09-410-194-21
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                                                                                                              SEQ ID NO 21
LENGTH: 571
TYPE: PRT
 Matches 109; Conservative
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                 Query Match
Best Local Similarity
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                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                    PRIOR FILING DATE: 1997-04-01 NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
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o. US20020095030A1
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Schneider, Pascal
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Burns, Kimberly
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                    26.4%;
29.9%;
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 61;
               Score 425.5; DB 10; Pred. No. 1.7e-35;
 Mismatches 110;
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US-09-227-721-12
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                                                                       GENERAL INFORMATION:
APPLICANT: Mark P. BOLDIN
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Yury V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ALDRESS:
                                                                                                                                                                                                                                      Sequence 30, Appli
Patent No. 6399327
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 EDSVDAKPDRSSFVPSLFSKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
 COUNTRY:
                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                          MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETD
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                 Washington D.C.
                                                                                                                                                                                                                                                        Application US/08983502
                                              419 Seventh Street N.W.,
USA
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                                                                 Browdy and Neimark
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                                               300
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RESULT 13
PCT-US96-10521-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 44.5%;
Best Local Similarity 50.5%;
Matches 143; Conservative 5
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WAI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 17-AUG-1333
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: IL 115,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                            233 MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                                                   259 MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
                                                                                                                                                                                                  199
                                                                                                                                                                                                                                                           139 CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
                                                                                                                                                                                                                                    116 CVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETD
                                                                                                                                                                                                                                                                                                                 56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
                                                                                                                                                                                                                                                                                                                                     79 DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                   19 EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 14-SE
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                              SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEI
                                                                                                                                                         SGVDDDMAC---HKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEF 232
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17-AUG-1995
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16-JUL-1995
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Sequence 30, Application PC/TUS9610521 GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-962-834A-2
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TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140, 431D2
CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 476
TYPE: DBT
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MEDLIN TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UNDER: US/09/962,834A

FILING DATE: 25-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: G15276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL PROTEASE NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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ZIP: 02140
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CITY: Cambridge
                                                                                                                               NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/675,123 FILING DATE: 1996-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
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Pred. No. 4.4e~35;
3; Mismatches 90;
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Search completed: December Job time: 9.35862 secs

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Matches 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                        444
469
                                                                                                                                              384
                                  287 QIPCVVSMLTKEL 299
                                                                                                            227
                                                                                                                                                                              169 DRCKTLLEKPKLFFIQACRGTELDDAIQADSGPINDTDA--NPRYKIPVEADFLFAYSTV 226
                                                                                                                                                                                                                    324 HNNVTKVEMEMVLQKQKCNPAHADGDCFVFCILTHGRFGAVYSSDEALIPIREIMSHFTA 383
                                                                                                                                                                                                                                                      111 YNDCSCAKMODLLKKAS-EEDHTNAACFACILLSHGEENVIYGKD-GVTPIKDLTAHFRG 168
                                                                                                                                                                                                                                                                                                269
                                                                                                                                                                                                                                                                                                                                                                     209 QGEEELVSQTDVKTFLEALPQESWQNKHAGSNGNRATNGAPSLVSRGMQGASANTLNSET
                                                                                                                                                                                                                                                                                                                                                                                                       11 QGVEDSANEDSV----DAKPDRS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                               51 TRDRVPTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 LVPRMLKFLEKTM 481
                                                                                                                                              LOCPRLAEKPKLFFIQACQGEEIQPSVSIEADALNPEQAPTSLQDSIPAEADFLLGLATV 443
                                                                                                                                                                                                                                                                                            STKRAAVYRMNRNHR--GLCVIVNNHSF---TSLKDRQGTHKDAEILSHVFQWLGFTVHI 323
                                                                        PGYVSFRHVEEGSWYIQSLCN---
                                                                                                          PGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 521 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: <Unknown>
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Pred. No. 2e-32;
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INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
MOLECULE TYPE: peptide
US-08-964-313-10
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 143; Conserv
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIL
OPERATING SYSTEM: DOS
                                          NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,125.
REFERENCE/DOCKET NUMBER: 19824Y
TELECOMUNICATION INFORMATION:
TELEPHONE: 732-594-4568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/030,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,313
FILING DATE: 04-NOV-1997
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US.
ZIP: 07065
                                                                                                                                                                                                                                                            79 DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03 -NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000 CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                            44.1%; Score 711; DB 3; Length 277; 50.5%; Pred. No. 2.2e-72; tive 50; Mismatches 78; Indels
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Search completed: December Job time: 16.1052 secs

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Result
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Maximum Match 100%
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

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US-08-964-308-10
US-08-964-313-10
US-08-964-313-5
US-08-96-227-721-21
US-08-96-227-731-21
US-08-96-227-813-4
US-08-96-885-5
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4	1, A	28,	27,	26	12	28,	26,	Sequence 12, Appl	Sequence 7, Appli	7	27,		ω	Sequence 2, Appli	Sequence 2, Appli	'n	Sequence 31, Appl

ALIGNMENTS

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US-08-462-969B-2
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US-08-462-969B-2
                  Query Match
Best Local Similarity
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                                                                                                                                                                                     TELEFAX: 301-309-8439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: He, We
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                   FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,969B
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleu
TITLE OF INVENTION: Like Apol
NUMBER OF SEQUENCES: 12
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                   TELEPHONE: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Ave. CITY: Rockville
                                                                                                                    STRANDEDNESS:
                                                                                                                                      TYPE:
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ZIP: 20850
                                                                                                                                                  LENGTH:
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linear
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Like Apoptosis Protease 3 and
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Score 1613; DB 3;
Pred. No. 1e-174;
); Mismatches 0;
                                  Length 303;
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APPLICANT: Alnemii, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                          SEQ ID NO 24
LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/09561756 Patent No. 6376226
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version
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                                  FVQALCSILEEHGKDLEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELY
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Pred. No. 6.4e-174;
1; Mismatches 1;
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US-09-227-721-24
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
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                                                                                                                                                                                                                                               Patent No. 6462175
GENERAL INFORMATION:
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Patent No. 6379950
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TITLE OF INVENTION: RECOMBLINANT,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/227,721 CURRENT FILING DATE: 1999-01-08
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                          APPLICANT: Armstrong, Robert APPLICANT: Tomaselli, Kevin TITLE OF INVENTION: Mch3, A TITLE OF INVENTION: Nucleic
                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICANT:
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                                                                           COUNTRY:
                                                                                                  STREET: 4370 La
CITY: San Diego
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                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                              , Application US/08556627A 6462175
                                                                                        California
                                                                                                              E: Campbell and Flores 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09227721
                                                                             USA
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                                                                                                                                                                                                              Litwack, Gerald
                                                                                                                                                                                                                                     Alnemri,
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Pred. No. 6.4e-174;
1; Mismatches 1;
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ds Encoding and Methods of Use
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                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08591605 Patent No. 6060238 GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619, 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: :
           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/591,605 FILING DATE: 09-FEB-1996
                                                                             COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                             APPLICANT: Dixit, Vishva M.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REGULATING
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
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LENGTH: 303 amino acic
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CLASSIFICATION:
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CITY: PALO ALTO
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                                                                  PatentIn Release #1.0, Version #1.30
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99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6066715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08964308
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: 2034-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
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                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
                                ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy |
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LENGTH: 277 amino acids
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REFERENCE/DOCKET NUMBER: 196
                                                                                                                         APPLICATION NUMBER: FILING DATE: 04-NOV
                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 07065
                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                       CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
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TOPOLOGY: linear
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                                                                                                                      04-NOV-1996
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50.9%; Pred. No. 1.6e-73;
50.9%; Mismatches 77;
                                                                                                                                          US/08/964,308
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RESULT 7
US-08-462-969B-4
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Best Local Similarity
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INFORMATION FOR SEQ
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                            REFERENCE/DOCKET NUMBER: PF
                                                                                                         FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
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TITLE OF INVENTION: Interlet
TITLE OF INVENTION: Like Apo
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                TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 05-JUN CLASSIFICATION: 514
                                                                             REGISTRATION NUMBER:
                                                                                                                        APPLICATION NUMBER: US 08/334,251 FILING DATE: 11-NOV-1994
                                                                                               NAME:
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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TYPE: amino acid
STRANDEDNESS: si
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                                                                                         Brookes, A. Anders
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Like Apoptosis Protease 3 and
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US-08-964-313-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6,
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Best Local Similarity
Matches 144; Conserv
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            APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPE L
REGISTRATION NUMBER: 35,125
                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/964,313
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                        COMPUTER: IBM CON
OPERATING SYSTEM:
REGISTRATION NUMBER: 35,125
                                                                                                                                                               FILING DATE: 04-NOV-1997
                                                                                                                                                                                                                                                                                                               COUNTRY:
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                  RAHWAY
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                                                                                                                                                                                                                                                                                                                 USA
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RAMACHANDRAN, CHIDAMBARAN
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50.9%; Pred. No. 1.6e-73;
... Mismatches 77;
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GENERAL INFORMATION:
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Best Local :
APPLICATION NUMBER: US/09/06
FILING DATE: 29-APR-1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., I.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
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STATE: NJ
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TELEFAX: 732-594-4720
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LEBLANC, YVES
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Pred. No. 1.6e-73;
Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 277
                                                                                                                                                                                       Matches 143;
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                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 63762
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12,
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                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/561,756 CURRENT FILING DATE: 2000-04-26
                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/227,721
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 480140.43
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                                                                                                                                                                                                                                                                                           TYPE: PRT
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LENGTH: 277 amino acids
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             139 CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
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                                               56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
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                                                                                                                                               19 EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF
                                                                                                                                                                                                     Match 44.5%;
Local Similarity 50.5%;
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                                                                                                                   ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF 55
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amino acid
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50.9%; Pred. No. 1.6e-73;
50.9%; Mismatches 77;
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                                                                                                                                                                                Score 718; DB 4; L
Pred. No. 3.5e-73;
Pred. No. 3.5e-77;
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RESULT 12
US-08-983-502-30
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US-09-227-721-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/227,721 CURRENT FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 480140.431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 27
TYPE: PRT
                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy an
                                                                                                    TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS TITLE OF INVENTION: AND OTHER PROTEINS NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                       259 MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
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STATE: I
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                                 CITY:
                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVINDCSCAKMQDLLKKASEEDHTNAACFA 138
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mes 143; Conserv
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                             Washington
                D.C.
                                               419 Seventh Street N.W.,
                                                                                                                                                                     Mark P. BOLDIN
Tanya M. GONCHAROV
                                                                                                                                                          Yury V. GOLTSEV
USA
                                                                                                                                                                                                             David WALLACH
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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 14-SEP-
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PRIOR APPLICATION DATA:
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                                                                                                                                 233 MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                               259 MOILTRVNDRVARHFESOSDDPHFHEKKQIPCVVSMLTKELYF 301
                                                                                                                                                                   139 CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
                                                                                                                                                                                                    56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
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                                                                                                                                                                                                                                                                                                     19 EDSYDAKPDRSSFYPSLFSKKKKNYTMRSIKTTRDRYPTYQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                          Local Similarity 50.5 es 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                       5 ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF 55
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                                                             DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
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SYSTEM: PC-DOS/MS-DOS
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50.5%; Pred. No. 3.5e-73;
rative 51; Mismatches 77;
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PCT-US96-10521-30

Sequence 30, Application GENERAL INFORMATION:

PC/TUS9610521

APPLICANT:

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US-08-964-308-10
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                                                                                                                                                   Patent No.
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Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                   Sequence 10,
                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-APR-1996 INFORMATION FOR SEQ ID NO: 3
          APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: IL 11
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 11
FILING DATE: 17-AUG-1995
CORRESPONDENCE ADDRESS
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APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CILLSHGBENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
                                                                                                                                                                                                                                                                                                                                      GVDDDMAC---HKIPVDADFLYAYSTAPGYYSWRNSKDGSWFTQSLCAMLKQYADKLEF 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF
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                                                                                                                                                                                                                                                                                                                                                                                SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEI 258
                                                                                                                                                     0, Application US/08964308 6066715
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; MOLECULE TYPE:
US-08-964-308-10
                                                                                  GENERAL INFORMATION:
APPLICANT: DESMACHA
APPLICANT: FRIESEN
APPLICANT: GRESSER
APPLICANT: KENNEDY
APPLICANT: NICHOLSC
APPLICANT: NAMACHAN
                                                                                                                                                                                                                           Sequence 10, Application US/08964313 Patent No. 6114132
                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 277 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
          TITLE OF INVENTION: PHOSPHATASE BINDING NUMBER OF SEQUENCES: 15
                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-7262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J
                                                                                                                                                                                                                                                                                                                                    233 MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                                                                                                                                                                                                                                                                                                              259 MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
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FILING DATE: 04-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
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GRESSER, MICHAEL
                                            SKOREY, KATHRYN
FORD-HUTCHINSON, ANTHONY
                                                                                                      NICHOLSON, DONALD
                                                                                                                          KENNEDY, BRIAN
                                                                                  RAMACHANDRAN, CHIDAMBARAN
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Pred. No. 2.2e-72;
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; STRANDEDNESS: single TOPOLOGY: linear , MOLECULE TYPE: peptide US-08-964-313-10
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INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
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Best Local Similarity 50.5
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATE O3 - NUV 17 FILING DATE: 03 - NUV 17 FILING DATE: 03 - NUV 17 FILING DATE: 04 - NUV 17 FILING DATE: NAME: DURETTE, PHILIPPE L. REGISTRATION NUMBER: 35,125 REFERENCE/DOCKET NUMBER: 19824Y TELECOMMUNICATION INFORMATION: "PPPPHONE: 732-594-4568"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,313
FILING DATE: 04-NOV-1997
CLASSIFICATION BATA:
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03-NOV-1996
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                                                 56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
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                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM CONTROL OPERATING SYSTEM:
SOFTWARE: FastSE
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Match Length
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-591-605-2
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US-08-964-313-6
US-09-964-313-6
US-09-961-756-12
US-09-961-756-12
US-08-983-502-30
PCT-US96-10521-30
US-08-964-308-10
US-08-964-313-10
US-08-965-756-34
US-09-561-756-34
US-09-561-756-34
US-09-561-756-35
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5.4 293 5.4 293 5.3 278 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 476 9.3 486 8.8 464 8.8 464 8.8 479 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 479 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 479 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 496 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 464 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 479 8.8 464 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 406 8.8 40	
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Patent No. 6066715
                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-7262
TELEFAX: 732-594-4720
121 TGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                   -964-308-6
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERT J.
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APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
                                       19
                                                                  61
                                                                                                                                                      Local Similarity
mes 277; Conserva
                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Version
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REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/964,308 FILING DATE: 04-NOV-1996
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                                                                                                    1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG 60
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                                                                                                                                                                                                                                                                                       ENGTH:
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                                                  MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                            MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                     MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG 60
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                                                                                                                                                                                                                                                                                   277 amino acids
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                                                                                                                                                               Score 1463; DB 3;
Pred. No. 1.7e-161;
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US-08-462-969B-4
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                                                                                                                                                                                                                                                                TOPOLOGY: 1. MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 11-NOV-1994
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OPERATING SYSTEM: PC-DA
SOFTWARE: PATENTIA Rela
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Interleu
TITLE OF INVENTION: Like Apo
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CORRESPONDENCE ADDRESS:
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CITY: Rockville
                                                                                       61
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                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
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DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN 240
                         HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
                                                                               MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                                                                                                                               al Similarity
277; Conserv
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Pred. No. 1.7e-161;
Mismatches 0;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03 -NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 19824Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4568
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                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
   61
                61 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                                                               Local Similarity les 277; Conserv
                                                                                                                                                                                                                                                                                                                                             TELEFAX: 732-594-4720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/964,313
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                                                                             1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
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MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
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                                                                                                                                 Conservative
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SKOREY, KATHRYN
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6 EAST LINCOLN AVENUE - P.O. BOX 2000
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MICHAEL
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                                                                                                                              Score 1463; DB 3;
Pred. No. 1.7e-161;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: FastSEQ for Windows V. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: YOUNG, ROBERT N.
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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              61 MTSRSGTDVDAANLRETERNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
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                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                      TYPE:
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TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 126 | CITY: RAHWAY
                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                   LENGTH:
                                                                           MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG 60
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MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
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FRIESEN, RICHARD
LEBLANC, YVES
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Pred. No. 1.7e-161;
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US-09-561-756-12
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   CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
                                                                                                                                         Sequence 12, Application US/09227721 Patent No. 6379950 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12
LENGTH: 277
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                                                                              APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09561756 Patent No. 6376226
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TITLE OF INVENTION: RECOMBINANT, ACTIVE CA
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
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ORGANISM: Homo sapien
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Pred. No. 3.7e-161;
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-12
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Patent No. 6399327
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Best Local Similarity
Matches 276; Conserv
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PRIOR APPLICATION NUMBER: IL 11
APPLICATION NUMBER: IL 11
APPLICATION NUMBER: IL 11
APPLICATION NUMBER: IL 11
                                                                                                                                                                         APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 16-JAN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DAVID WALLACH
APPLICANT: MARK P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Yury V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                             STREET: 419 Seven CITY: Washington STATE: D.C.
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                                                                                                    FILING DATE:
                                                                                                               APPLICATION NUMBER:
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                                                                                                  17-AUG-1995
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                                                                                                                                               16-JUL-1995
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Pred. No. 3.7e-161;
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PCT-US96-10521-30
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Best Local Similarity
Matches 276; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 1
FILING DATE: 16-JUL-1995
                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                    FILING DATE: 17-AUG-
PRIOR APPLICATION DATA:
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                     APPLICATION NUMBER: FILING DATE: 27-DE
                                                                    APPLICATION NUMBER: FILING DATE: 14-SEP
                                                                                                                    APPLICATION NUMBER: IL 1: FILING DATE: 17-AUG-1995
                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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STRANDEDNESS: sir
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                                                                    TUMBER: IL 115,319
                     27-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.8%; Score 1460; DB 4; 99.6%; Pred. No. 3.7e-161;
                                    IL 116,588
                                                                                                                                   IL 114,986
                                                                                                                                                                                        IL 114,615
                                                                                                                                                                                                                                                           PCT/US96/10521
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    Mismatches

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                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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RESULT 10
US-08-964-308-10
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                                                                                                                                                                                                                                                                                                                                                                            CIP: U/VU-
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Diskette

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FastSEQ for Windows Version 2.

CURRENT APPLICATION DATA:

CORRENT APPLICATION NUMBER: US/08/964,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 276; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J
REGISTRATION NUMBER: 27,366
REGISTRATION NUMBER: 198
REFERENCE/DOCKET NUMBER: 198
TELECOMMUNICATION INFORMATION:
TELEDHONE: 732-594-7262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERT J. NORTH - MERCK & CO.,
STREET: 126 EAST LINCOLN AVENUE - P.O. BO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FRIESEN, RICHARD
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
TELEPHONE: /32 - TELEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 04-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 126 | CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
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STRANDEDNESS: sir
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Pred. No. 3.7e-161;
1; Mismatches 0;
                                                                                                                                                            19840 PCT
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STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: peptic
US-08-964-308-10
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US-08-964-313-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                    FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03 -NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: DURESTE, PHILIPPE L.
                                                                                                                                                               SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO.,
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
          NAME: DURETTE, PHILIPPE L. REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                                           APPLICATION NUMBER: 60/030,408
                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>5</del>
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o. 6114132
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                                                                                                                                                                                                                                                                                                            RAHWAY
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                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                FRIESEN, RICHARD
GRESSER, MICHAEL
KENNEDY, BRIAN
                                                                                                                                                                                                                                                                                                                                                                           FORD-HUTCHINSON, ANTHONY VENTION: PHOSPHATASE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                      RAMACHANDRAN, CHIDAMBARAN
                                                                                                                                                                                                                                                                                                                                                                                                            SKOREY, KATHRYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESMARAIS,
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Pred. No. 2
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Patent No.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT:
                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE
                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              APPLICANT: YOUNG, ROBERT N.
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
NUMBER OF SEQUENCES: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                             NAME: DURETTE, PHILIPPE REGISTRATION NUMBER: 35,
                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                      COUNTRY: US
ZIP: 07065
                                                                                          APPLICATION NUMBER: FILING DATE: 29-APF
                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                    CITY: RAHWAY
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TYPE: amino acid
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                                                                                      JMBER: US/09/069,138
29-APR-1998
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99.6%;
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Pred. No. 2.4e-160;
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Best Local Similarity
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INFORMATION FOR SEQUENCE CHARA
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                        REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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TELEFAX: 7
TELEX:
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                                                                                                                                                                                                                                                                                STREET: Lilly Corp
CITY: Indianapolis
STATE: Indiana
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                           APPLICATION NUMBER: US/08/890,542A FILING DATE: 09-JUL-1997 CLASSIFICATION: 435
                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                              TELEFAX:
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    CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          Lilly Corporate Center
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                (317) 276-3861
OR SEQ ID NO: 2:
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linear
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99.6%;
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US-09-561-756-34
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                                                                                                                                                                                                                                                                SEQ ID NO 34
LENGTH: 290
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                    Query Match
Best Local :
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Best Local Similarity
                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alnemii, Emad S.
TITLE OF INVENTION: RECOMBLIANT, ACTIVE CASPASES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
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                                                                                                                                                                                    Local Similarity
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HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETD 290
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Pred. No. 4.9e-143;
                                                                                                                                                                     Score 912; DB 4;
Pred. No. 1.7e-97;
0; Mismatches 0;
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RESULT 15 US-09-227-721-34

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Requence 34, Application US/09227721

Patent No. 637950

GRNERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: THEREOF
ITTLE OF INVENTION: THEREOF
ITTLE OF INVENTION: THEREOF
ITLE FEBRENCE: 480140, 431

CURRENT PILING DATE: 1999-01-08

NUMBER OF SED ID NOS: 116

SOFTMARE: FASTSEQ for Windows Version 3.0

LENGTH: 290
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequ
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Minimum DB
Maximum DB
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Maximum Match 10
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10 US-09-809-905-2

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US-09-895-263-4
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Sequence 9, Appli	equence 18, App	e 47950,	equence 27, App	equence 15,	e 14, App	e 34,	e 15, App	24, App	•	5, Appl	2, Appl	(D	, Appl	2, Appl	e 24,	36, App	e 48728,	e 21, App	e 2, Appl	e 9, Appl	e 28, Āpp	e 2,	equence 20, App	equence 33,	~

ALIGNMENTS

Sequence 4, Application US/09895263
Patent No. US20020076793A1
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
Like Apoptosis Protease 3 and 4 REFERENCE/DOCKET NUMBER: PF140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-251-6015
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS: APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119 ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/895,263
FILING DATE: 02-Jul-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA: MOLECULE TYPE: protein CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sc
STREET: 9410 Key West Ave. NUMBER OF SEQUENCES: 12 STATE: MD COUNTRY: U STRANDEDNESS: single TYPE: amino acid TOPOLOGY: CITY: Rockville LENGTH: 277 amino acids USA linear Genome Sciences, Inc

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US-09-895-263-4
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Matches
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TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431D2
CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09954697
Patent No. US20020106631A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
                                                                                                                                                                                                                                           Query Match
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TYPE: PRT
                                                                                                                                                                                                                                                                           ORGANISM: Homo sapien
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hes 277;
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                                                                                                                                                                      1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
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         RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                               HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                             MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                                                                        MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                                                  HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
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Pred. No. 2.1e-136;
1; Mismatches 0;
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Pred. No. 1.1
0; Mismatches
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1.1e-136;
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RESULT 3

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1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKWDYPEWGLCIIINNKNFHKSTG 60

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CURRENT APPLICATION NUMBER: US/09/954,69
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTMARE: FastSEQ for Windows Version 3.
SEQ ID NO 34
LENGTH: 290
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COUNTY OF THE PROPERTY OF THE PROPERTY ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 264
; TYPE: PRT
; ORGANISM: HOMO S
US-10-103-448-3
                                                             ; OTHER INFORMATION: Rev-Caspase-3 contructed from human caspase US-09-954-697-34
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                   Query Match
Best Local S
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       Matches
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Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                                     TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES TITLE OF INVENTION: THEREOF FILE REFERENCE: 480140.431D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wu, Joseph C.
TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3,
TITLE OF INVENTION: COMPRISING THE SAME AND ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 480140.468D1
CURRENT APPLICATION NUMBER: US/10/103,448
CURRENT FILING DATE: 2002-03-20
NUMBER OF SEQ ID NOS: 7
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                   Similarity
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Fritz, Lawrence C.
   62.3%;
Conservative
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                                                                                                                                                                                                          US/09/954,697
   Score 912; DB 10;
Pred. No. 2.2e-82;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1397; DB 9;
Pred. No. 3.1e-130;
1; Mismatches 0;
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                              Length 290
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    Indels
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RESULT 6
US-09-809-905-2
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                                    ; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-905-2
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     Query Match
                                                                                                      SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09809905 Patent No. US20020001806A1
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                 APPLICANT: Huang, Yuanhui
APPLICANT: Sun, Yi
APPLICANT: Wang, Kevin Ka-Wang
TITLE OF INVENTION: CASPASE-3S SPLICING VI
FILE REFERENCE: U.S. Application A0000224
CURRENT APPLICATION NUMBER: US/09/809,905
CURRENT FILING DATE: 2001-03-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES TITLE OF INVENTION: THEREOF FILE REFERENCE: 480140.431D2
                                                                                                                                     PRIOR APPLICATION NUMBER: 60/204,468 PRIOR FILING DATE: 2000-05-16 NUMBER OF SEQ ID NOS: 5
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CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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     56.9%;
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   Score 833;
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Pred. No. 7.9e-81;
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 DB 10;
Length 182;
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                                                                                    Matches 145;
                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQ 161
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                                     5 ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/556,627
FILING DATE: 13 NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/944,851
FILING DATE: 31-Aug-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Mch3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alnemri, Emad S
EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
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                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619) 535-90
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Diego
                                                                                                                                                                                                                                                                   LENGTH: 303 amino acids
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P-ID 1813
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                                                                                    Conservative
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Tomaselli, Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Litwack, Gerald
                                                                                                     49.6%;
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                                                                                    49;
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                                                                                                   Score 725; DB 10;
Pred. No. 6.1e-64;
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; Mismatches 0;
                                                                                Mismatches
                                                                                                                        DB 10;
                                                                                                                   Length 303;
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HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115

Version #1.30

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US-09-895-263-2
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US-09-954-697-24
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                                                                                                                                         Sequence 2, Application US/09895263
Patent No. US20020076793A1
GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 303
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TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT FILING DATE: 2001-09-14
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                            NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                            AL INFURDATION:
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 Beta Converting
Tike Apoptosis Protease 3 and
                                                                                                                                                                                                                                                                                                                                           SGPINDTDANPRYKIPYEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKDLEI
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CITY: Rockville
                   STREET:
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               9410 Key West
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                                                                                       Enzyme
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US-09-954-697-21
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                                                                          GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431D2
CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 21
LENGTH: 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Sim
Matches 144;
                                                                                                                                                                                                           Sequence 21, Application UPatent No. US20020106631A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 301-251-6015
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                            259
                                                                                                                                                                                                                                                                                                                                               233 MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                      MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDSVDAKPDRSSFVPSLESKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/895,263 FILING DATE: 02-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            Application US/09954697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jonathan L. Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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Pred. No. 1.5e-63;
i0; Mismatches 77;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                     Matches 103;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES TITLE OF INVENTION: THEREOF FILE REFERENCE: 480140.431D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alnemri, Emad S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 476
TYPE: PRT
445 YEVSNK-----DDKKNMGKQMPQPTFTLRKKLVF 473
                                         241
                                                                                                                                                       325
                                                                                                                                                                                                                                                                                                             205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 CFASMLTKKLHFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 CIVSMLTKELYFY 276
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                             19 KIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKST-----GMTSRSGTDVDA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                                                                                                                                                                                                                                               72 ANLRETFRULKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 YKMDHRRRGIALIFNHERFFWHLTLPERRGTCADRDNLTRRFSDLGFEVKCFNDLKAEEL 96
                                                                                                                                                                     G-PVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGI--ETDSG----VDDDMAC 184
                                                                                                                                                                                                                             GALTTTFEELHFEIKPHHDCTVEQIYEILKIYQLMDHSNMDCFICCILSHGDKGIIYGTD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSHRETVNGSWYIQDLCEMLGKYGSSLEFTELLTLVNRKYSQRRVDFCKDPSAIGKKQVP
                                     RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                         POTRYIPDEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILTEVN
                                                                                                           HK---IPVEADELYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADK-LEFMHILTRVN 240
                                                                                                                                                 GQEAPIYELTSQFTGLKCPSLAGKPKVFFIQACQGDNYQKGIPVETDSEEQPYLEMDLSS
                                                                                                                                                                                                                                                                                                       KIINDYEEFSKGEELCKVYQMKSKPRGYCLIINNHNFAKAREKVPKLHSIRDRNGTHLDA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFIIQACRGTELDCGI------ETDSGVDDDMACHKIPVEADFLYAYSTAPGY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLKIHEVSTVSHADADCFVCVFLSHGEGNHIYAYDAKIEIQTLTGLFKGDKCHSLVGKPK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPK 156
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37.5%;
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                                                                                                                                                                                                                                                                                                                                                                                 Score 429; DB 10;
Pred. No. 1.7e-34;
9; Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 476;
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RESULT 12

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APPLICANT: Heinrikson, Robert I.

APPLICANT: Tomasselli, Alfredo G.

APPLICANT: Tomasselli, Alfredo G.

FILE OF INVENTION: Method for Autoactivation of Procaspase 8

FILE REFERENCE: Docket No. US20020045205A1 6172

CURRENT APPLICATION NUMBER: US/09/862,915

CURRENT FILING DATE: 2001-05-22

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

SEQ ID NO 1
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SEQ ID NO 20
LENGTH: 479
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Best Local Similarity
                                                                                                            NUMBER OF SEQ ID NOS: 27 SOFTWARE: FastSEQ for Wi
                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 1999-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
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APPLICANT: Thome, N
APPLICANT: Burns, F
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Rimoldi, Donata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bodmer, Jean- Luc
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Conservative 4
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; Pred. No: 3.2e-34;
49; Mismatches 96;
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; ORGANISM: Homo sapiens US-09-410-194-20

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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-952-768-4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 102;
                                                                                                                       TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/952,768
FILING DATE: 10-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chitchianco Unition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273
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                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 480140.424C4 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Alnemri, Emad S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADK-LEFMHILTRVNRKVAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFEELHFEIKPHDDCTVEQIYEILKIYQLMDHSNMDCFICCILSHGDKGIIYGTDGQEAP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNG-PVD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPDEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILTEVNYEVSN 452
                                               TOPOLOGY: linear
                                                                     TYPE: amino acid
                                                                                                                                                                                                                            NAME: Christiansen, William T.
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Seed Intellectual Property Law Group STREET: Suite 6300, 701 Fifth Avenue
                                                                                                                                                                                                            REGISTRATION NUMBER: 44,614
                                                                                                                                                          TELEPHONE: (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVENTION: MCH4 AND MCH5, NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomaselli, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Armstrong, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Litwack, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fernandes-Alnemri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.8%;
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Pred. No. 1e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Srinivasula, Srinivasa M.
APPLICANT: Fernandes-Alnemi, Teresa
APPLICANT: Fernandes-Alnemi, Teresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10068569 Patent No. US20020160975A1
                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 480140.475
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 416
TYPE: PRT
ORGANISM: Homo sapiens
   390
                                      242
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                                                                                                          183
                                                                                                                                             270
                                                                                                                                                                                                                                                                                150 DLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTA 209
                                                                                                                                                                           146 DRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDDDM-----
                                                                                                                                                                                                              210 KKMYLALLELAQQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDGCPVSVEKIVNIFNG
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                                                                                                                                                                                                                                                                                                                   34 DNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 EFESFSEDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 TFEELHFEIKPHHDCTVEQIYEILKIYQLMDHSNMDCFICCILSHGDKGIIYGTDGQEAP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 TFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNG-PVD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 SESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKST-----GMTSRSGTDVDAANLRE 76
   AVSVK---
                                 KVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                    DAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVAN
                                                                                                                                      TSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQL 329
                                                                                                                                                                                                                                               EEIVELMRDVSKEDHSKRSSFVCVLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGI--ETDSG----VDDDMACHK---
                                                                                                     -ACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADK-LEFMHILTRVNRKVAT
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--GIYKQMPGCFNFLRKKLFF
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37.8%;
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                                                                                                                                                                                                                                                                                                                                                      Score 417; DB 9;
Pred. No. 2.1e-33;
1; Mismatches 90
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Pred. No. 1.1e-33;
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Search completed: December Job time: 8.64138 secs

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Minimum DB
Maximum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                         Score
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-895-263-4
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                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995_DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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                 AAE00600
ABJ01218
                                                   AAW00372
AAW00677
AAR95831
AAW41688
AAW16600
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AAU05394
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                                                                                                                                                                                                                                          SUMMARIES
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                                                                                                                                                                                                                                                                        score distribution.
                                                                                                                                                                                                                                                                                       chance to have a result being printed,
                                                                                                                                                                                     Description
               Human caspase-3.
Human caspase-3 SE
                                                   Human caspase
                                                               Amino acid sequenc
Apopain CPP32a pro
Amino acid sequenc
                                                                                                                    Pro-Yama. Homo sa
Human interleukin-
                                                                                                                                                    Apopain CPP32beta
apopa
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sequen	AAY21720	20	293		525.5
Mouse caspase 6 pr	AA021924	23	276		526
Recombinant CPP-32	AAU79218	21	107	٠	551
Human interleukin-	AAR95830	17	341	9.	582
Caspase-7. Uniden	AAB98655	22	244	9.	723.5
caspa	ABB09300	23	336	9	725
Human caspase 7 pr	ABB09299	23	303	9	725
caspas	ABB09297	23	303	9.	725
caspase-7	ABJ01222	23	303	9.	725
Human caspase-7.	AAE00604	22	303	9.	725
id seque	AAY21721	20	303	49.6	725
tic proteas	AAW15262	18	303	9	725
ine proteas	AAW15247	18	303	9.	725
caspase 7	ABB09298	23	340	1.	48
e casp	ABB78588	23	303	ŗ	748.5
-HER2	AAB82925	22	527	2	98
Anti-HER2 HuMab4D5	AAB82924	22	513	2	9
Amino acid sequenc	ABB09606	23	182	6.	833
	ABJ01227	23	285	1	896
o acid sequen	AAY21726	20	. 285	۲.	896
-rearranged	AAU80040	22	556	ш	900
rearranged c	AAU97935	22	556	-	900
milk	AAU80335	22	559	2	912
Fab/C	AAU80038	22	559	۲.	912
Fab1	AAU97946	22	559		912
Rev-c	ABJ01226	23	290	٧.	912
acid s	AAY21725	20	290	۲.	912
meric cas	AAE00610	22	261	σ.	1271.5
se-3. Un	AAB98654	22	241	7.	* 1
an caspas	AAB59579	22	245	7	~
se caspase 3.	0539	22	277	œ	1293
a a	71	22	277	œ	1296
nterleukin-1	4708	19	277	9	1304
caspase-	67	21	249	90.4	1322
Mutant human apopa	AAW48937	19	277		1453

ALIGNMENTS

RESULT 1 AAW00372

AAW00372 standard; protein; 277

AΑ

26-JUN-1997 AAW00372;

(first entry)

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cleavage enzyme; human; monocytic leukaemia; cell line; rHP-1; ldentification; modulator; recombinant production; gene therapy; pro-inflammatory; pro-apoptotic; apoptosis; inflammation; antibody; antisense DNA; treatment; immune; proliferation; degeneration; disease; AIDS; acquired immunodeficiency syndrome; autoimmune; pathogenic infection; cardiovascular; neurological; injury; alopecla; ageing; cancer; type I diabetes; Parkinson's; Alzheimer's.
                                                                                                             Key
Domain
  Cleavage-site
                                                                                                                                                                                                                                                                                      CPP23beta; isoform; inactive; CPP32; proenzyme; cysteine; protease; proteolytic product; poly(DP-ribose) polymerase; PARP; apppain;
                                                                    Cleavage-site
Region
                            Protein'
                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                  Apopain CPP32beta proenzyme.
29..175
/note= "17 kDa subunit p17"
175..176
                                                                    /note=
28..29
29..46
                                                                                                               Location/Qualifiers
1..28
                                                       /note=
                                       "amino-terminal sequence determined
  purified enzyme subunits"
                                                                                               "amino-terminal pro-domain"
                                                         for
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The present sequence is the CPP23beta or Glu190 isoform of the CP inactive CPP32 proenzyme (a member of the interleukin converting cenzyme/pro-apoptotic protein CED-3 family of cysteine proteases of CC unknown function cloned from Jurkat cells), the proteolytic product CC of which is the poly(DP-ribose) polymerase (PARP) protease, apopain. The PARP cleavage enzyme was purified from the human CC monocytic leukaemia cell line, THP-1, using standard ion exchange CC chromatography techniques and SDS PAGE. Apopain can be used to CC identify apopain activity modulators, while apopain encoding DNA CC may be used for apopain production or in gene therapy (i.e. in vivo CC or ex vivo gene transplantation) for enhancing the pro-inflammatory CC or pro-apoptotic effects of apopain. Anti-apopain antibodies and CC antisense DNA can be used to reduce or eliminate the CC of apopain activity is beneficial in the treatment of immune, CC disease, pathogenic infections, cardiovascular and neurological continuous and neurological infections, cardiovascular and neurological and particon's
                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 277
                                                                                                                                                                                                                                                                                                                         Sequence
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     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apopain, a new human apoptosis related enzyme - responsible for the proteolytic breakdown of poly(ADP- ribose) polymerase (PARP) which
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                                                                                                                                                                                                                                                      Local 5.
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                                                                                                                                                                                                                                                                                                                                                  ary, alopecia, ageing Alzheimer's disease
                       RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
                                                                                             HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                       MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                                                                                      MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                                                                                 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
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) MERCK FROSST CANADA INC.
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller DK, Nicholson DW,
                                                                                                                                                                                                                                                                                                                        277 AA;
                                                                                                                                                                                                                                                              100.0%;
ilarity 100.0%;
Conservative (
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purified enzyme subunits"
165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis
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                                                                                                                                                                                                                                                                                                                                                              cancer,
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Pred. No. 1e-147;
% Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                           type I diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pentapeptide containing putative cysteine"
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                                                                                                                                                                                                                                                                                   Human pro-Yama (AAW00677) is a zymogen which upon activation cleaves PARP to an 85 kDa form. Activated Yama has the ability to modulate cellular function associated with the Fas receptor pathway such as Fas-associated apoptosis. This activity is inhibited by CrmA (see also AAW00678). The pro-Yama sequence was deduced from a cDNA clone isolated from human umbilical vein endothelial cells. Yama can be produced in a host cell and used to modulate cellular function, to raise antibodies, or to screen for agents or drugs which modulate
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding Yama protein or CrmA mutant -modulating apoptosis, maintaining {\tt T} cell viability in Al and for drug screening
       181
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13-FEB-1995;
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                                                                                                                                                               1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
              DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                             HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                               HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
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277; Conserv
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95US-0389812.
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Pred. No. le-147;
Mismatches (
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                                                                                                                                                                                                                                                                                                                                   This ICE-LAP-4 protein may be used therapeutically, e.g. as an antitumor or antiviral agent and to control embryonic development and tissue homeostasis. The protein can also be used to treat immunosuppression disorders, such as AIDS, by targeting virus infected cells for cell death. The DNA may find use in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ICE-LAP-3 and -4 DNA and protein - useful in the diagnosis and treatment of Alzheimer's disease, Parkinson's disease, rheumatoid arthritis, septic shock and head injury
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 44; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-239509/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1994;
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enzyme; Alzheimer's disease; Parkinson's disease; septic shock;
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                                                                                                    121 HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
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                                                                                                                                                       MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
              RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
                                    MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
                                                                                       HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
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applications.
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                                                                                                                                                                                                                                                                                                    277 AA;
                                                                                                                                                                                                                                               100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    He W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0334251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US07235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hudson PL,
                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277
                                                                                                                                                                                                                                                             Score 1463;
Pred. No. le
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA;
                                                                                                                                                                                                                                                            1e-147;
                                                                                                                                                                                                                                                                         DB 17;
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                                                                                                                                                                                                                                                                          277;
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                                                                                                                                          120
                                                                                                                                                                                              60
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Дb
241 RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
 277
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RESULT 4
AAW41688
CrmA; tumour necrosis factor receptor; TNF-R; U1-70; apoptosis; activation; U1-70 path; apoptosis path; id
                                                                                                                                                                        modulation.
                                                                                                                                                                                                   02-JUL-1998
                                                                                                                                                                                                             AAW4 1688
                                                                                                                                                                                          Amino acid sequence of a protein designated YAMA
                                                                                                                                                                                                                      AAW41688 standard; Protein;
                                                                                                                                                                                                   (first
                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                      277
                                                                                                                                                                            0; inhibition;
identification;
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Synthetic. 25-NOV-1997. JP09299077-A

27-JAN-1997; 09-FEB-1996; 96US-0591605 97JP-0012932

Controlling apoptosis by inhibiting activation of the U1-70 pathway - by introduction of nucleic acid encoding protein with CrmA biological activity into the cell

N-PSDB;

1998-056551/06 DB; AAV05471.

(UNMI) UNIV MICHIGAN

Disclosure; Fig 2; 48pp; Japanese.

designated YAMA. The specification describes a novel method of controlling cell functions controlled by the tumour necrosis factor receptor (TNF-R) pathway containing U1-70. The method comprises introducing a nucleic acid molecule encoding CrmA into a cell, and culturing the cell under suitable conditions for transcription and translation of the CrmA nucleic acid. Method for preventing and inhibiting apoptosis by inhibiting activation of the U1-70 path, identifying the chemical related to the apoptosis path, and screening candidate chemical having biological function in the apoptosis path ar also described. The methods can be used to identify substances which modulate apoptosis in cells controlled by the TNF-R pathway. are

Sequence 277 AA;

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                                                                                                                                      1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
                                         DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                                                             MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                  MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                                                            MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
                                                                                                                                                                                 Similarity
                                                                                                                                                                       Conservative
                                                                                                                                                                                100.0%;
                                                                                                                                                                    0;
                                                                                                                                                                                Score 1463; DB 19; Length 277; Pred. No. 1e-147;
                                                                                                                                                                       Mismatches
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181

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The present sequence is the CPP23a or Asp190 isoform of the inactive CPP32 proenzyme (a member of the interleukin converting enzyme/pro-apoptotic protein CED-3 family of cysteine proteases cunknown function cloned from Jurkat cells), the proteolytic prod of which is the poly(DP-ribose) polymerase (PARP) protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPP23a; isoform; inactive; CPP32; proenzyme; cysteine; protease; proteolytic product; poly(DP-ribose) polymerase; PARP; apopain; cleavage enzyme, human; monocytic leukaemia; cell line; THP-1; identification; modulator; recombinant production; gene therapy; pro-infiammatory; pro-apoptotic; apoptosis; inflammation; antibody; antisense DNA; treatment; immune; proliferation; degeneration; disease; AIDS; acquired immunodeficiency syndrome; autoimmune; pathogenic infection; cardiovascular; neurological; injury;
                                                                                               Apopain, a new human apoptosis related enzyme proteolytic breakdown of poly(ADP- ribose) polym
                                                                    Claim 1;
                                                                                                                                                         Ali A,
                                                                                                                                                                                                                                 17-APR-1996;
                                                                                                                                                                                                                                                        24-OCT-1996
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                                                                                                                                                                                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW16600 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apopain CPP32a proenzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lopecia; ageing; cancer; type I diabetes; Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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                                                                                                                                                                             MERCK
                                                                                                                                                                                         MERCK
                                                                  Page -; 84pp; English.
                                                                                     the onset of apoptosis
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                                                                                                                                                                            FROSST CANADA INC.
                                                                                                                                                                                         & CO INC
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175..176
176..193
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28..29
29..46
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                        Nicholson DW,
                                                                                                                                                                                                                                                                                                                                                                                                "17 kDa subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "amino-terminal pro-domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                "amino-terminal
                                                                                                                                                                                                                                                                                                "12 kDa subunit p12"
                                                                                                                                                                                                                                                                                                                                                              "amino-terminal sequence
                                                                                                                                                                                                                                                                                                                                "conserved
                                                                                                                                                                                                                                                                                                                      catalytic
                                                                                                                                                                                                                                                                                                                                                     purified
                                                                                                                                                                                                                                                                                                                                                                                                                      purified enzyme
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                                                                                                                                                                                                                                                                                                                                                     enzyme
                                                                                                                                                                                                                                                                                                                      pentapeptide containing putative
cysteine"
                                                                                                                                                      Thornberry NA,
                                                                                                                                                                                                                                                                                                                                                                                                p17"
                                                                                                                                                                                                                                                                                                                                                                                                                              sequence determined
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                                                                                               yme · responsible polymerase (PARP)
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rev-caspase; cysteine protease; zymogen; caspase; autoimmune disease; caspase-mediated apoptosis; ne tumour cell; myocardial infarction; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apopain. The PARP cleavage enzyme was purified from the human monocytic leukaemia cell line, THP-1, using standard ion exchange chromatography techniques and SDS PAGE. Apopain can be used to identify apopain activity modulators, while apopain encoding DNA may be used for apopain production or in gene therapy (i.e. in vivo or ex vivo gene transplantation) for enhancing the pro-inflammatory or pro-apoptotic effects of apopain. Anti-apopain antibodies and antisense DNA can be used to reduce or eliminate the
                                                                                                         Alnemri ES;
                                                                                                                                                                                                             09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                         WO9935277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                  11-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY21717 standard; Protein; 277
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                                                                                                                                                        (UYJE-) UNIV
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Pred. No. 2.2e-147;
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WPI; 1999-419353/35 N-PSDB; AAX81219.

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cells transfected with a rev-caspase expressing vector can be used in identification of inhibitors or enhancers of caspase-mediated apoptosis. In vitro translated rev-caspase can be used to identify an inhibitor or enhancer of caspase processing activity. Caspase inhibitors are useful for treating neurodegenerative diseases as well as for inhibiting apoptosis in the heart following myocardial infarction. Sequences AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10 gene products (AAY21715-Y21724).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rev-caspases are cysteine proteases that specifically cleave proteins after Asp residues and is expressed as a zymogen, in which the small subunit is N-terminal to a large subunit. A gene delivery vehicle comprising a rev-caspase coding sequence is useful for the treatment of cancer, where the gene delivery vehicle is internalised by tumour cells. The gene delivery vehicle can also be used to treat autoimmune diseases.
                                                                                                                                                                                                                                                                                                                   AAU05394 standard; Protein; 277
            18-JAN-2000; 2000US-0484617
                                          11-JAN-2001; 2001WO-US00888
                                                                        26-JUL-2001
                                                                                                    WO200153310-A1
                                                                                                                                  Homo sapiens
                                                                                                                                                               atherosclerosis;
                                                                                                                                                                            Human; caspase 3;
viral infection; l
                                                                                                                                                                                                                         Human caspase 3
                                                                                                                                                                                                                                                         24-OCT-2001
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                                                                                                                                                            ; apoptosis; hyperproliferative disorder; hepathaematopoietic disorder; autoimmune disorder. neurological disorder.
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Pred. No. 2.2e-147;
1; Mismatches 0;
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                                                     Cleavage-site
                                                                                                                                                                                         Human; caspase-3; CPP32; yama; apopain;
cysteine protease; apoptosis; caspase expression cassette; metastasis;
tumour; cathepsin B; urokinase; proliferation; gene therapy.
                                                                                                                                                                                                                                                                                                     Human caspase-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE00600 standard; Protein;
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DB; AAS10503.
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276; Conserv
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28..29
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9..10
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2.2e-147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC CP932, yama and apopain. Caspases are a family of cysteine proteases, cc that participate in the initiation and execution of apoptosis. Caspases cc exist as pro-enzymes, activated by cleavage into a large and small closupartic aspuratic acid residues within the pro-enzyme sequence. The present invention relates to a method for cc functional cloning of genes encoding proteins or enzymes involved in cc pro-enzyme sequence. The invention is based on the use of caspase cc expression cassettes comprising the coding sequence of a proteolytic cleavage aite flanked by sequences encoding sequence of a proteolytic cleavage site flanked by sequences encoding sequence of a proteolytic cleavage site flanked by sequences encoding two caspase subunit. A cc fusion polypeptide comprising a first and a second caspase subunit, and cc cloning gene encoding enzymes involved in proteolytic cleavage. An cc expression cassette containing fusion polypeptide is used to identify a cutant cell line deficient in an enzyme of interest and is also useful cc alignosis and suppression of proliferation or metastases of a tumour cell characterised by overexpression of a polypeptide (e.g. Cathepsin B course) in a metastase of a tumour coll characterised by overexpression of a polypeptide). DNA encoding fining relations a metastase of a time of the containing the containing colling the containing colling the containing colling the containing the containing colling colling the containing colling the containing colling the containing colling the colling the colling colling the colling colling the colling colling the colling the colling colling the colling colling the colling the colling colling the colo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion
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14-AUG-2000;
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Pred. No. 2.2e
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2.2e-147;
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RESULT

RESULT 10 AAW48945 ID AAW48 XX

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of human rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences can be used in the gene therapy of cancer and autoimmune diseases. The present sequence is a protein described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New rev-caspases engineered to contain the small subunit fused in N-terminal to the large subunit, which is in reverse order to the
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08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention
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                        RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                      HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
                                                                                                                                                                                                                                                                               MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
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DB; ABT03966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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autoimmune disease; cytostatic; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 13; 81pp; English
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99US-0227721.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1460; D
Pred. No. 2.2e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treat cancer and autoimmune diseases
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Best Local S
Matches 276
                                                                                                                                                                                                                                                                  using mutated proceases and phosphatases whereby the catalytic cysteine residue of the enzymes are replaced with a serine or alanine residue to correct the problem of interference in SPA from extraneous oxidising and alkylating agents. The mutation affects the catalytic properties of the enzyme but does not affect their binding properties. The invention provides for new ligands for use in SPA which have increased binding affinity for a tyrosine phosphatase or cysteine protease. The ligands contain at least two 4-phosphono(difluoromethyl) phenylalanine groups which increase binding affinity of the ligand to its respective enzyme. The assay can be used to determine the ability of new ligands and compound mixtures to competitively bind with an enzyme. The method is claimed to allow a better usage of SPA in the discovery of compounds for the treatment and study of diseases, e.g. diabetes, cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a mutated human apopain (caspase-3) C163S pro-enzyme. The active enzyme containing P17 subunit (Ser29-Asp175) and P12 subunit (Ser176-His277) was engineered for expression using the MetSer29-Asp175 and MetSer176-His277 constructs. The invention claims for a method for use in a scintillation proximit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzyme binding assay for detection of useful compounds - uses mutant form of wild-type enzyme, in which serine replaces cysteine at active site, to reduce interference from oxidising/alkylating agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention claims for a method for use in a scintillation binding assay (SPA) for proteases and phosphatases. The method for the second protection of the second protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Pages 39-40; 63pp; English.
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Kennedy B, Nicholson
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                                                                                                                                                                                                 Sequence
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1 Similarity
276; Conser
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                                                                                        Conservative
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163
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176..277
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Pred. No. 1.2e
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Skorey
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The present sequence represents a mutated human apopain (caspase-3) C163S pro-enzyme. The active enzyme containing P17 subunit (Ser29-Asp175) and P12 subunit (Ser176-His277) was engineered for expression using the MetSer29-Asp175 and MetSer176-His277 constructs. The invention provides a method for use in a scintillation proximity binding assay (SPA) for proteases and phosphatases. The method invol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant human apopain pro-enzyme; caspase-iscintillation proximity binding assay; dia 4-phosphono(difluoromethyl) phenylalanine
                                                                                                       Peptide(s) useful in binding assays for tyrosine phosphatases or cysteine proteases - contain two or more 4-phosphono(difluoromethyl) phenylalanine groups to improve binding affinity
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                                                                                  Disclosure;
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163
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                                                                                                                                                                                                                                                                                                                                                 Cys in wild-type to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes; cancer;
ine group; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pro-enzyme
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   The method involves
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RESULT 12
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Best Local S
Matches 276
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             Judgement of apoptosis-controlling activity for selecting drugs can be used for preventing and treating various diseases caused abnormality in apoptosis control -  \frac{1}{2} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB26763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB26763 standard;
                                                                                                                                                             WPI; 2000-605051/58
                                                                                                                                                                                                                                                                                         29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                     29-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caspase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis; detection; Nrf2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human caspase-1 protein sequence
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                                                                                                                                                                                                                      (SUMO ) SUMITOMO CHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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276; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
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                                                                                                                                                                                                                                                                                     99JP-0022356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
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Pred. No. 1.2e-146;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevention;
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                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
AAW47089
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A method for identifying drugs which exhibit apoptosis-controlling activity involves the use of a human Nrf2 protein. Nrf2 is a caspase substrate. The method involves detecting cleavage of the Nrf2 protein by caspase in the presence of a candidate drug. Detection of cleavage of the Nrf2 protein by caspase in the presence of a candidate drug indicates apoptosis inducing activity. The method can be used for selecting a drug which can be used for the prevention and the treatment of various diseases caused by abnormality in apoptosis control, such as cancer. The
                      N-PSDB; AAV13959
                                                                                                                                                                                                                                                                   Interleukin-1 beta converting enzyme related protease; ICE related protease; rat; apoptosis; inhibitor; brain ischaemia; Alzheimer's disease; amyotrophic lateral sclerosis; head trauma;
                                                                                                                     22-JUL-1996;
                                                                                                                                              15-JUL-1997;
                                                                                                                                                                          29-JAN-1998
                                                                                                                                                                                                  WO9803642-A1
                                                                                                                                                                                                                                                        neurodegenerative
                                                                                                                                                                                                                                                                                                                         Rat interleukin-1 beta converting enzyme-related
                                                                                                                                                                                                                                                                                                                                                     20-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                          AAW47089 standard; Protein; 277
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                                                                                          (ELIL ) LILLY &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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                                    1998-120767/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTKELYFYH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSLTGKPKLFIIQACRGTELDCGIETDSGVDDDMACHKIPVEADFLYAYSTAPGYYSWRN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDLTREEIVELMRDVSKEDHSKRSSFVCYLLSHGEEGIIFGTNGPVDLKKITNFFRGDRC 148
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                                                                                                                                                                                                                               qs
                                                               Paul SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 13; 17pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AA;
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                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Pred. No. 1.1e-132;
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Rat interleukin-1 beta converting enzyme related protease -

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RESULT 14
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AC AAG78
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Best Local S
Matches 245
  (NORQ ) NORINSUISANSHO KACHIKU EISEI.
(MUNE/) MUNETA Y.
(MORI/) MORI Y.
                                                                                                    05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG78712;
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                                                                                                                                                   03-OCT-2000; 2000JP-0303931
                                                                                                                                                                                                                                                       JP2001169785-A
                                                                                                                                                                                                                                                                                                       Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                        Pig caspase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rat brain cDNA library. ICE related protease is present central nervous system and is enriched in central neurons.
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Pred. No. 1e-130;
3; Mismatches 1
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Best Local
                                                                                                                                                                                     Mouse; caspase 3; apoptosis; hyperproliferative disorder; hepatitis; viral infection; haematopoletic disorder; autoimmune disorder;
                           Zhang H,
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(ARAI/)
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                                                                                          11-JAN-2001; 2001WO-US00888
                                                                                                                                    WO200153310-A1
                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                     Mouse caspase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural gene of swine caspase family, used inflammatory reactions in infectious diseases
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245; Conserv
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) ARAI K.
                                                ISIS PHARM INC
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                            Cowsert LM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  in an invention relating to novel antisense oligonucleotides (AAS10517-AAS10676) and methods of using these compounds for the modulation of caspase 3 expression. The caspase 3 antisense oligonucleotides specifically hybridise with and inhibit the expression of caspase 3. Antisense compounds targeted to caspase 3 are useful to inhibit caspase 3 expression in cells or tissues and to modulate apoptosis. The caspase 3 antisense oligonucleotides are useful for treating disorders associated with expression of caspase such disorders include hyperprollferative disorders (e.g. cancer) viral infections (e.g. hepatitis), haematopoletic disorders, autoimm
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's disease).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 96-97; 127pp; English.
New antisense compound to inhibit caspase {\mathfrak Z} is useful for treating hepatitis and atherosclerosis -
                                                                                                                                                                                  277 AA;
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Gapop 10.0 , Gapext 0.
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2172.860 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671580
      O98ui8 brachydanio
O91b65 xenopus lae
O88550 rattus norv
O99m47 mus musculu
O9bqe7 homo sapien
O91889 oncorhynchu
O91b66 xenopus lae
O94089 mus musculu
O93615 gallus gall
                                                                                                                                      Q96an1 homo sapien
Q96kp2 homo sapien
Q95nd5 sus scrofa
Q9qwi4 mus musculu
                                                                                                               093417 gallus gall
077623 ovis aries
                                                                                                                                                                                                  Description
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Q96AN1 RESULT 1

Q96AN1; Q96AN1; 01-DEC-2001 01-DEC-2001 01-MAR-2002

PRELIMINARY;

PRT;

Hypothetical

(TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
1 31.6 kDa protein.

45	44	43	42	41	40	39	38 8	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
283	302.5	306.5	306.5	310.5	310.5	324	325	327.5	328.5	349	360	374.5	383.5	404	417	421	421	422	422	422.5	423	431.5	432.5	434	435	436	437.5	484
19.3	0	۲.	۲.	•	•	22.1	•	٠	•	•	•		•	27.6	•		•										29.9	33.1
383	347	826	263	536	268	423	393	452	435	479	417	520	500	403	416	538	496	308	308	476	399	131	482	454	480	454	482	326
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Q99M88	Q9GV89	Q9Y055	Q9TZP5	018203	Q9TZP6	Q9IB67	Q9R0S9	055194	Q9BUP7	80AM80	091106	Q9IB62	Q9IB64	Q90WU0	Q9BQ62	Q8TDI5	Q9C0K4	Q9VET9	Q9NHF9	Q918J3	Q9IB63	Q9CXM4	Q90WU1	Q9ЛНК1	089110	Q9R0T0	Q9JНX4	Q9GV88
8	Q9gv89 hydra atten	Q9y055 caenorhabdi	Q9tzp5 caenorhabdi	018203 caenorhabdi	Q9tzp6 caenorhabdi .		Q9r0s9 mus musculu	4 rat	homo		pristion	xenopus		0 gal	homo	homo	homo	Q9vet9 drosophila	Q9nhf9 drosophila	brachyda	xen		gallus		E C		4 ratt	Q9qv88 hydra atten

ALIGNMENTS

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                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 277; Conservative 0;
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Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; ILLECENZYME.
PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (NOV-2001) to the
EMBL; BC016926; AAH16926.1;
InterPro; IPR002398; ICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                               Hypothetical protein. SEQUENCE 277 AA; 31608 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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IPR002138; ICE_p10.
IPR001309; ICE_p20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                         Score 1463; DB 4;
Pred. No. 1.6e-114;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                  2F35CD3BCF7FF64A CRC64;
                                                                                                                                                                                                                                Length
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RESULT
Q96KP2
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ID DT Q1
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Best Local S
Matches 272
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Pfam; PF00656; ICE_p20; 1.

PROM; PR00376; ILIBCENZYME.

PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.

PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.

PROSITE; PS50207; CASPASE_P10; 1.

PROSITE; PS50208; CASPASE_P20; 1.

SEQUENCE 277 AA; 31642 MW; 6162767B0D2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Control of the activation of the procaspase-3 by a at the N-terminus of the p17 subunit."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databa EMBL; AJ413269; CAC88866.1; - IRR003398; ICE.
InterPro; IPR002338; ICE_p10.
InterPro; IPR002318; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; |
NCBI_TaxID=9606;
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Q96KP2;
O1-DEC-2001
O1-DEC-2001
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             181
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MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
                                                                           MTSRSGTDVDAANLRETERNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
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Metazoa; Chordata; C
Metazoa; Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (TrEMBLrel. 19, 11 (TrEMBLrel. 19, 12) (TrEMBLrel. 20, 12)
                                                                                                                                                                                                                                                                                                                  Conservative
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Last sequence
Last annotation
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Pred. No. 1.1e
2; Mismatches
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Catarrhini;
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i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                    DB 4;
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RESULT

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Best Local S
Matches 245
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InterPro; IPRO02139; ICE_p20.
Pfam; PP00655; ICE_p20; 1.
Pfam; PP00655; ICE_p20; 1.
Pfam; PP00656; ICE_p20; 1.
PROSITE; PS01122; CASPASE_UTS; UIPROSITE; PS01121; CASPASE_HIS; UIPROSITE; PS01127; CASPASE_P10; 1
PROSITE; PS02007; CASPASE_P10; 1
PROSITE; PS02008; CASPASE_P20; 1
PROSITE; PS02008; CASPASE_P20; 1
                                                                                                         Q9QWI4;
Q9QWI4;
01-MAY-2000
01-MAY-2000
01-JUN-2002
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                   CPP32 apoptotic
                                                                        CASP3
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01-DEC-2001
01-DEC-2001
01-JUN-2002
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"Porcine caspase-3: cloning and its activity during porcine PKI5 cells induced by porcine Fas-ligand.";

J. Interferon Cytokine Res. 21:409-415(2001).

EMBL; AB099345; BAB55544.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-21334413; PubMed-11440638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
                                                                                                                                                                                                                                                                                                                         RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
                                                                                                                                                                                                                                                                                                                                                                                                       DMACHKIPVBADELYAYSTAPGYYSWRNSKDGSWEIQSLCAMLKQVADKLEEMHILTRVN
                                                                                                                                                                                                                                                                                                   RKVAVEFESFSTDSTFHAKKQIPCIVSMLTKELYFYH
                                                                                                                                                                                                                                                                                                                                                                                    DMACQKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAALKQYVHKLELMHILTRVN
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                                                                                                      0 (TrEMBLrel. 13, 0 (TrEMBLrel. 13, 2 (TrEMBLrel. 21,
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(TrEMBLrel. 19,
(TrEMBLrel. 21,
                                                                                                                                                                                                PRELIMINARY;
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                                                                                       protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.6%;
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                                                                                       (Fragment)
                                                                                                         Last sequence up
                                                                                                                                                  Created)
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Pred. No. 1.5e
11; Mismatches
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Last sequence
Last anno
  Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                PRT;
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616C0F56141B012B
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Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
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Sus.
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RESULT
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Best Local Similarity
Matches 191; Conserv
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InterPro; IPR002138; ICE_p10.
InterPro; IPR001399; ICE_p20.
InterPro; IPR001399; ICE_p20.
InterPro; ICE_p10; 1.
InterPro; ICE_p20; 1.
INTERPROSTOR ILIBCENZYME.
SMART; SM00115; CASC; 1.
INTERPROSTOR IN
                                                                                                                                                                                                                                                                                                                                                                                                      O93417;
01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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  InterPro; IPR002398;
InterPro; IPR002138;
InterPro; IPR001309;
                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01122; CASPASE_CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20;
                                                              Biol. Reprod. 62:589-598(2000).
EMBL; AF083029; AAC32602.1; -.
HSSP; P42574; IPAU
MEROPS; C14.003; -.
                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20149872; PubMed=10684799;
Johnson A.L., Bridgham J.T.;
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                           Caspase-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; C14.003; -. MGD; MGI:107739; Casp3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Denis F., Alam A., Cohen L., Hartgers F., Braun M., Mar
Fortin J.-P., Sekaly R.-P.,
"Multiple Pathways of Apoptosis Converging on the CPP32
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                    cells."
                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
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HSSP; P42574; 1PAU.
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                                                                                                                                                                      Caspase-3 and
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                                                                                                                                                                        -6 expression and
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ICE_p10.
ICE_p20.
                                       ICE.
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Pred. No. 2.9e
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FE7F4857C4EBA544 CRC64;
                                                                                                                                                                    enzyme activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283
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ches 11;
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InterPro; IPR002398; ICE.
InterPro; IPR002188; ICE_p10.
InterPro; IPR001309; ICE_p20.
InterPro; IPR001309; ICE_p20.
InterPro; IPR001309; ICE_p20; 1.
Pfam; PF00655; ICE_p10; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01121; CASPASE_CYS; 1
PROSITE; PS01121; CASPASE_HIS; 1
PROSITE; PS50207; CASPASE_P10; 1
PROSITE; PS50207; CASPASE_P10; 1
PROSITE; PS50207; CASPASE_P10; 1
PROSITE; PS50207; CASPASE_P20; 1
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1 1
SEQUENCE 182 AA; 20408 MW; B
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077623;
01-NOV-1998 (TIEMBLrel. 08, C
01-NOV-1998 (TIEMBLrel. 08, L
01-MAR-2002 (TIEMBLrel. 20, L
Caspase-3 (Fragment).
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SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_HIS; 1
PROSITE; PS01121; CASPASE_HIS; 1
PROSITE; PS50207; CASPASE_P10; 1
PROSITE; PS50208; CASPASE_P20; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rueda B.R., Hendry I.R., Tilly J.L., Hamernik D.L.;
"Accumulation of Caspase-3 mRNA and Induction of Caspase Activity
the Ovine Corpus Luteum Following Prostaglandin-F2a Treatment In
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF068837; AAC25713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vivo.
                                                                                                                                                                                                                                                                                                                                             MEROPS; C14.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF068837;
HSSP; P42574; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKIPVEADFLYAYSTAPGYYSWRNAAEGSWFIQSLCRMLKEHARKLELMQILTRVNRRVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Pred. No. 2.9e
43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
     B5860C6996C21BE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161242DDEFD4DC4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
2.9e-72;
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Query Match

58.4%;

Score 854;

DВ

6;

Best

Local Similarity

87.4%;

Pred. No.

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RESULT 7
098UT8
ID 098UT8
AC 098U
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                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                      Matches 149;
                                                                                                                                                                                                                                                                                                                       Priam; PF00655; ICE_P10; 1.

Priam; PF00656; ICE_P20; 1.

Prints; PR00376; ILIBCENZYME.

SMART; SM00115; CASC; 1.

PROSITE; PS01122; CASPASE_P15; UNKNOWN_1.

PROSITE; PS01121; CASPASE_H15; UNKNOWN_1.

PROSITE; PS010207; CASPASE_P10; 1.

PROSITE; PS50208; CASPASE_P20; 1.

SEQUENCE 282 AA; 31522 MW; 13C3454F5E099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q98UI8;
Q98UI8;
Q1-JUN-2001
Q1-JUN-2001
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caspase-3.
                                                  , 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002398; ICE_p10.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalian
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Yabu T., Okazaki T., Yamashita M.;
"Molecular Cloning and Gene Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2000) to the EMBL; AB047003; BAB32409.1; HSSP; P42574; IPAU.
            160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZFIN; 2DB-GENE-011210-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS;
                                                                                          100
                                                                                                                             97
                                                                                                                                                                       40
                                                                                                                                                                               37 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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LFIIQACRGTELDCGIETDSGVDDDM--ACHKIPVEADFLYAYSTAPGYYSWRNSKDGSW
                                                                             YSLNYPNIGHCIIINNKNFDRRTGMNPRNGTDVDAGNVMNVFRKLGYIVKVYNDQTVAQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLDNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDL 91
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caspase-3."
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l (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                 53.5%;
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17,
21,
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                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                            Score 782; DB 13;
Pred. No. 1.5e-57;
32; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) (Zebra danio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                         1.
13C3454F5E09932E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.2e-64;
ches 11;
                                                                                                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                      282;
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RESULT 8
Q91B65
ID Q91B
AC Q91B
AC Q91B
AC Q91B
Casl
OT 01-C
DT 01-C
DT 01-C
DT 01-C
Euk
OC Euk
OC Amp
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OC Amp
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RESULT
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Best Local S
Matches 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002398; ICE
InterPro; IPR002138; ICE
InterPro; IPR001309; ICE
Pfam; PF00655; ICE_D10;
Pfam; PF00655; ICE_D20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSO1122; CASPASE_CYS; PROSITE; PSO1121; CASPASE_HIS; PROSITE; PSSO207; CASPASE_P20; PROSITE; PSSO208; CASPASE_P20; SEQUENCE 318 AA; 35937 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-20209426; PubMed-10744739;
Nakajima K., Takahashi A., Yaoita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00376; ILIBCENZYME SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; C
Amphibia; Batrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; C14.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB038170; BAA
HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XCASPASE-7.
Xenopus laevis (African clawed frog).
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                                                                                      264
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"Structure, expression and function o
                                                                                                                                                                                                                                                                                                                                                            84
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                                                                            NEYGKELEVMQILTRVNFLVATQFESYSDDPQFSKKKQIPCVVSMLTKELYF
                                                                                                      KQYADKLEEMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                                                                                                                  DGLEADSGSVNDSLETDANPRHKIPVEADFLYAYSTVPGYYSWRNPGMGSWFVQALCSVL
                                                                                                                                                                                              KRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELD
                                                                                                                                                                                                                                                                                                                                                                            INNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHS
                                                                                                                                                                                                                                                                                                                                                                                                                                         EEGEDSVDAKPDRSQRFSIFSSTKKKKVEDKPPKTNNNVRIVTPAFQYKMNNGNVGRCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENTENSVDSKSIKNLEPKIIHGSESM---DSGISLDNS----YKMDYPEMGLCII 49
                                                                                                                                                                                                                                                             DSACFACIFLSHGEEGLIYGTDGAMPIKVLTTLFRGDNCRSLVGKPKLFFIQACRGHEFD
                                                                                                                                                                                                                                                                                                                                                 INNKIFDKITGMGARNGTDIDARELLRCFKGLGFDVNVYNNKSCEEMENLLRTVAQQDHK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275:10484-10491(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAA94748.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ICE_p10.
ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15,
15,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 761; DB 13,
Pred. No. 1e-55;
Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6EBC6684AF86A128 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caspase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                     263
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AC DT DAY OCCUPANTS OF THE STANDARD SOUTH OF

1;

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RESULT 10
Q99M47
ID Q99M4
AC Q99M4
AC Q99M4
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-MA
CASPA
GN CASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10
InterPro; IPR0031309; ICE_p20
InterPro; IPR001309; ICE_p20
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                         01-JUN-2001
01-JUN-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01122; CASPASE_CYS; PROSITE; PS01121; CASPASE_HIS; PS0207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20; SEQUENCE 303 AA; 34324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Rat caspase-7 sequence.";
Submitted (JUN-1998) to the
EMBL; AF077124; AAC24011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
       Strausberg R.;
                           SEQUENCE FROM N.A
                                                                                                                                                       caspase 6.
                                                                                                                                                                                                                                                     Q99M47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00376; IL1BCENZYME. SMART; SM00115; CASc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Rat caspase-7 se
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caspase-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forghani F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               088550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; C14.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDSGVDDDMAC---HKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIMQILTRVNDRVARHFESQSDDPRFNEKKQIPCMVSMLTKELYF 301
                                                                                                                                                                                                                                                                                                                                                                  EFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                                                                                                                                                                                                                                                                                 ADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRNPGKGSWFVQALCSILNEHGKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STEDGVDAKPDRSTIISSLLWKKKNASMCPVSTTRDRVPTYLYRMDFEKMGKCIIINNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTENSVDSKS-----IKNLEPKIIHGSESMDSGISLDN----SYKMDYPEMGLCIIINNK 53
                                                                                                                                                                         l (TrEMBLrel.
l (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 (TrEMBLrel. 8 (TrEMBLrel. 9 (TrEMBLrel. 9 )
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                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICE_p10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.9%;
53.7%;
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17,
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                                                                                                                                                                       Last sequence up
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Last seq
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                                                                                                                                                                                                              Created)
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 745; DB 11;
Pred. No. 2.1e-54;
1; Mismatches 79;
                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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A71728754BF199DD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BQET;
Q9BQET;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
InterPro; IPR002398; ICE_p10.
InterPro; IPR002138; ICE_p20.
InterPro; IPR001309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                             Submitted (NOV-2000) to the EMBL; BC004460; AAH04460.1; EMBL; BC000305; AAH00305.1; HSSP; P42574; 1PAU.
                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                          SEQUENCE FROM
TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BQE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSO1122; CASPASE_CYS; PROSITE; PSO1121; CASPASE_HIS; PSS0207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20; SEQUENCE 276 AA; 31563 MW;
                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                    Strausberg
                                                                                                                                                                                                                                                                                                      TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC002022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1312921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFIIQACRGSQHDVPVVPLDVVDHQTDKLDNVTQVDAASVYTLPAGADFLMCYSVAEGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKMDHKRRGVALIFNHERFFWHLTLPERRGTNADRDNLTRRESDLGFEVKCFNDLRAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVSMLTKELYF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHRETVINGSWYIQDLCEMLARYGSSLEFTELLTLVINKKVSQRRVDFCKDPDAIGKKQVPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P42574;
                                                                                               C14.005;
                                                                                                                                                                                                                                                                 (MAR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH02022
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                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                 б
                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 526; DB 11;
Pred. No. 3.8e-36;
2; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 1.
; 1.
; 1.
5965C5932A127B6C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
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                                                                         R InterPro; IPR002398; ICE_pl0.
R InterPro; IPR002138; ICE_pl0.
R InterPro; IPR002138; ICE_p20.
R InterPro; IPR001309; ICE_p20.
R Pfam; PF00655; ICE_p20; 1.
R Pfam; PF00656; ICE_p20; 1.
R PRNSTS; PR00376; ILLBCENZYME.
R SMART; SM00115; CASC; 1.
NR PROSITE; PS01112; CASPASE_CYS; 1.
NR PROSITE; PS01112; CASPASE_HIS; 1.
NR PROSITE; PS01121; CASPASE_HIS; 1.
NR PROSITE; PS01207; CASPASE_P10; 1.
NR PROSITE; PS02008; CASPASE_P20; 1.
SR PROSITE; PS02008; CASPASE_P20; 1.
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Matches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                           Laing K.J., Holland J., Bonilla S., Cunningham C., "Cloning and sequencing of caspase 6 in rainbow tromykiss, and analysis of its expression under conditinduce apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID-8022;
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01-MAR-2002 (TrEMBLrel.
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    ocal Similarity
109; Conserved
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E; PS01121; CASPASE_HIS; 1
E; PS50207; CASPASE_P10; 1
E; PS50208; CASPASE_P20; 1
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         Conservative
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  Score 525.5; |
Pred. No. 4.7e
63; Mismatches
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Last sequence update)
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Pred. No. 4.
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    . 4.7e-36;
tches 97;
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Gaps
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01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00376; ILIBCENZYME SMART; SM00115; CASC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-20209426; PubMed=10744739;
Nakajima K., Takahashi A., Yaoita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB038169;
HSSP; P42574; 10
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Xenopus laevis (African clawed frog).
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                                                                                                                                                                        VELDPSAEYIMTHKRRGLALIFNHEDFYWQLRLGSRRGTNTDSMNLNRILTDLGFDVQNY 101
                                                                            YNLRTMDVLEKIQEASTTDHSNADCFLCVFLSHGEDKHIYSYDSLIDIQELTNPFKGDKC
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                                                                                                                                                                                                                                                                                                                                                                         3; PS01122; CASPASE_CYS; J

3; PS01121; CASPASE_HIS; J

4; PS50207; CASPASE_P10; J

5; PS50208; CASPASE_P20; J

1E 303 AA; 34132 MW; 4
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chem.
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1CP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275:10484-10491(2000).; BAA94747.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICE_p10.
                                                                                                                                                                                                                                                                                                               35.8%;
                                                                                                                                                                                                                                                                                                    42.4%;
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15,
20,
                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                           Score 524; DB 13;
Pred. No. 6.3e-36;
8; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                         4C54A0A607C69756 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                           14;
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                              197
                                                                            161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
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RESULT 14
Q9D089
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kadoki J., Fukuda S.,
RA Arakawa T., Saito R., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kudota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                       Matches
                                                                                  Query Match
                                                                                                                                                                                                      InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
InterPro; IPR001309; ICE_P20.
Pfam; PF00655; ICE_P10; 1.
Pfam; PF00656; ICE_P20; 1.
                                                                                                                                        PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TREMBLrel. 17, Created)
01-JUN-2001 (TREMBLrel. 17, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
10 days embryo cDNA, RIKEN full-length enriched library,
clone:2610037G10, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9D089;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9D089
                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
EMBL; AK011710; BAB27792.1; -.
HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE-EMBRYO; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                               PRINTS; PR00376; ILIBO SMART; SM00115; CASC;
                                                                                                                                                                                                                                                                                MGD; MGI:1312921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CASP6
                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 GKKQIPCFASMLTKKLF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 KSLYGKPKIFILQACRGEKHDEPYLPKDEYDSYPLTNYTEYDAASLC-TLPAGADFIMCY
                             37
  20
                                                                       Local
                      YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAEGYYSHRETVNGSWYIQDLCAVYKAYAASLEFTEILTLVNRKVSQRSVEYCNDPKAI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFH 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKKQIPCIVSMLTKELY 274
 YKMDHKRRGVALIFNHERFFWHLTLPERRGTNADRDNLTRRFSDLGFEVKCFNDLRAEEL 79
                                                                                                          2; PS01122; CASPASE_CYS; 1

2; PS01121; CASPASE_HIS; 1

2; PS50207; CASPASE_P10; 1

3; PS50208; CASPASE_P20; 1

3; PS50208; CASPASE_P20; 1

2E 276 AA; 31591 MW; 5
                                                                     Similarity
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                             IL1BCENZYME
                                                                                                                                                                                                                                                                             Casp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                    35.3%;
41.0%;
                                                      42;
                                                      Score 516; DB
Pred. No. 2.6e
12; Mismatches
                                                                                                       ; 1.
; 1.
; 1.
; 1.
597EDF2321126B6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276
                                                      DB 11;
.6e-35;
les 94;
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                                                                               Length 276;
                                                      Indels
                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus.
                                                    Gaps
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093415
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                                                                                                          Matches
                                                                                                                                    Query Match
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01-NOV-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          093415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caspase-6
                                                                                                                                                                                                                                                                                                                  MEROPS; C14.005
                                                                                                                                                                                                                                                                                                                                 HSSP; P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11953316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200
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                         97
                                                    49
                                                                                                                       Loca:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FASMLTKKLHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVSMLTKELYF
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Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Caspase-6 gene disruption reveals a requirement for lamin A cleavage in apptotic chromatin condensation."; EMBO J. 21:1967-1977(2002).
EMBL; AF082329; AAC32378.1; -.
EMBL; AF469049; AAL82386.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-20149872; PubMed-10684799;

Johnson A.L., Bridgham J.T.;

"Caspase-3 and -6 expression and enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                      PROSITE; PS01122; CASPASE_CYS;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
SEQUENCE 304 AA; 34534 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Reprod. 62:589-598(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruchaud S., Korfali N., Villa P., Kottke T.J., Dingwall
Kaufmann S.H., Earnshaw W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002138;
InterPro; IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002398;
109 LKKVFEASRDDYSNADCFVCVFLSHGENDHVYAYDAQIKIETITNMFRGDKCQSLVGKPK 168
                                                                                                                         37 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                       VELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPK 156
                                                                                  YKMNHQRRGVALIFNHEHFFWHLRLPDRRGTLADRNNLKRSLTDLGFEVRIFDDLKAEDV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHRETVNGSWYIQDLCEMLARYGSSLEFTELLTLVNRKVSQRRVDFCKDPDAIGKKQVPV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFIIQACRGSQHDVPVVPLDMVDHQTDKLDNVTQVDAASVYTLPAGADFLMCYSVAEGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFIIQACRGTELDCGIETDSGVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLKIHEVSTSSHIDADCFICVFLSHGEGNHVYAYDAKIEIQTLTGLFKGDKCQSLVGKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (TrEMBLrel. 08, 0
3 (TrEMBLrel. 08, 1
2 (TrEMBLrel. 21, 1
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1PAU.
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                                                                                                                                                                                                                                                                                                                                                                                                                         ICE_p10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                      35.2%;
                                                                                                                                                                   46;
                                                                                                                                                                   Score 515; DB
Pred. No. 3.6e
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                      1.
1.
51CE31EBCAAE7383 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DDMACHKIPVEADFLYAYSTAPGYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity
                                                                                                                                                                                                            DB
                                                                                                                                                                                         6e-35;
                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                     92;
                                                                                                                                                                                                          Length 304;
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                                                                                                                                                                     Indels
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                                                                                                                                                                     12;
                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
                                                                                                                                                                   μ,
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Qy Db Searc Job t	ОУ	Оy
Qy 265 IVSMLTKELYFY 276 : : Db 289 FASMLTKKLYFH 300 Search completed: December 2, 2002, 12:58:11 Job time: 27.2672 secs	205 SWRNSKDGSWFIOSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPC 264 : : : :	157 LFIIQACRGTELDCGIETDSGVDDMACHKIPVEADFLYAYSTAPGYY 204

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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A;Accession: I39005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-189, 'E',191-277 <RES>
A;Cross-references: EMBL:UZ6943; NID:g857568; PIDN:AAA74929.1; PID:g857569
C;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte
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A;Residues: 29-46;176-189,'E',191-193 <NIC>
R;Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poiri Cell 81, 801-809, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:U13737; NID:g561665; PIDN:AAA65015.1; PID:g561666 R;NiCholson, D.W.; All, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant; Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A;Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammal A;Reference number: S58899; MUID:95319529; PMID:7596430
A;Accession: S58899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
C;Accession: A55315; S58899; I39005
R;Fernandes-Alnemri, T; Litwack, G:; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A;Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elega A;Reference number: A55315; MUID:95074098; PMID:7983002
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A;Molecule type: mRNA
A;Residues: 1-277 <FER>
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Matches 276
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                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                                                                                                                                                                                                                                            MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG 60
                                                                                 HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
                                                       HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 99.8%; Score 1460; DB 2;
99.6%; Pred. No. 2.1e-111;
Live 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 277;
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RESULT 2
S04710
Cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
Cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
Cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
Cysteine proteinses cricetulus griseus (Chinese hamster)
Cysteine proteins griseus (Chinese hamster)
Cysteine proteins (Srestin 13-mar-1997 #text_change 05-Nov-1999
Cysteine protein griseus (Chinese hamster)
Cysteine protein griseus griseus (Chinese hamster)
Cysteine protein griseus gris
A; Molecule type: mRNA
A; Residues: 1-277 <MUK>
A; Cross-references: DDB:
A; Experimental source: 6
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JC5410
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                                                                                                                            Blochem Biophys. Res. Commun. 231, 770-774, 1997
A;Title: Specific expression of CPP32 in sensory neurons
A;Reference number: JC5410; MUID:97224429; PMID:9070890
A;Accession: JC5410
                                                                                                                                                                                                                        C;Accession: JC5410
R;Mukasa, T.; Urase, K.; Momol, M.Y.; Kimura,
                                                                                                                                                                                                                                                                  C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change
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                                                                                                      A; Status: nucleic acid sequence
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caspase-9 long chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-2001 #sequence_revision
C;Accession: JC7123
R;Fujita, E.; Jinbo, A.; Matuzaki, H.;
                                                             RESULT
JC7123
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A;Accession: 167437
A;Status: preliminary; translated from GB/I
A;Molecule type: mRNA
A;Residues: 1-212 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cysteine proteinase (EC 3.4.22.-) P32 - r
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-7ul-1996 #sequence_revision 26
C;Accession: I67437
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167437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Interleukin-1-beta-converting enzyme-related proteases nulosa cells of the ovarian follicle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Endocrinology 136, 5042-5053, 1995
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Best Local Similarity
Matches 242; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                      Similarity
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87.7%;
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                                                                                                                                                                                                                                                                                                                      Score 996;
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P32 - rat (fragment)
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Pred. No. 8.
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                       23-Mar-2001
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                                                                                                             212
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                       #text_change
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                       23-Mar-2001
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Konishi,

н.,

Kikkawa,

protein

similar

to mammalian

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RESULT 6
G02635
ICE-LAP6 - human
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C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G02635
R;Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, V submitted to the EMBL Data Library, April 1996
A;Reference number: H01513
A;Accession: G02635
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A;Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027
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A; Residues: 1-416 < DUA>
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A;Residues: 1-454 <FUJ>
A;Cross-references: DDBJ:AB019600; NID:g6440941; PID:g6440942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9 A;Reference number: JC7123; MUID:20001956; PMID:10529400
A;Accession: JC7123
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    DNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93
                             AVSVK - -
                                                                                                                                                                                                                       DRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDDDM----
                                                                                                                                                                                                                                                                             KKMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDGCPVSVEKIVNIFNG
                                                                                                                                                                                                                                                                                                                                                          DLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRRRESSLHFMVEVKGDLTA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVSEK-----GTY---KQIPGCFNFLRKKLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DMAYTLDSDPCGHCLIINNVNFCRSSGLGTRTGSNIDRDKLEHRFRWLRFMVEVKNDLTA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRCRSLTGKPKLFIIQACRGTELDCGIET----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKMVTALMEMAHRNHRALDCFVVVILSHGCQASHLQFPGAVYGTDGCSVSIEKIVNIFNG
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                                                                KVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                                                                                                                                              TSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAVSSLPTPSDILVSYSTFPGFVSWRDKKSGSWYIETLDGILFQWARSEDLQSLLLRVAN 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGCPSLGGKPKLFFIQACGGEQKDHGFEVACTSSQGRTLDSDSEPDATPFQEGPRPLDQL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEIVELMRDVSKEDHSKRSSFVCVLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 145
                                                                                                          DAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVAN
                                                                                                                                                                                                                                                                                                                      EEIVELMRDVSKEDHSKRSSFVCVLLSHGEE------GIIFGTNG-PVDLKKITNFFRG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ACHKIPVEADELYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNR 241
                                                                                                                                                   -ACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                           -GIYKQMPGCFNFLRKKLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                             28.6%; Score 418; DB 2; 33.2%; Pred. No. 2.2e-26; tive 51; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.9%; Score 437; DB 2 36.1%; Pred. No. 7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: A49429;
R; Yuan, J.; Shaham, Cell 75, 641-652, 199
A; Title: The C. elega
                                                                                                                                                                                                                              hypothetical protein C48D1.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T20038 R;Burton, J.
A; Experimental source:
C; Genetics:
A; Gene: CESP: C48D1.2
A; Map position: 4
                                                                                                        A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-495 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;TILLE: The C. elegans cell death gene ced-3 encodes a A;Reference number: A49429; MUID:94061982; PMID:8242740 A;Accession: A49429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 *sequence_revision 18-Nov-1994 *text_change 01-Dec-2000
C;Accession: A49429; T37312
R;Yuan, J; Shaham, S; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
                                                                                                                                                                        A; Reference number: A; Accession: T20038
                                                                                                                                                                                          submitted to the EMBL Data Library, A; Reference number: 219214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: sequence extracted A; Accession: T37312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:L29052; NID:g6503232; PIDN:AAA27982.2; PID:g6503233
A;Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBIP:139826)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-503 <YUA>
                                                                                                                                                                                                                                                                                                                                         T20038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                          YFW 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPAFLRRGWDNRDGPLFNFLGCVRPQVQQVWRKKPSQADILIAYATTAQYVSWRNSARGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEEGIIFGTNG-PVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVD- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRDFAKHE-SHGDSAILVILSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WFIQAVCEVFSTHAKDMDVVELLTEVNKKVACGFQT---SQGSNILKQMPEMTSRLLKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WFIOSLCAMLKOYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKOIPCIVSMLTKEL
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                                                                                   EMBL: Z81049; PIDN: CAB02848.1; GSPDB: GN00022; CESP: C48D1
                                                                  clone C48Dl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.1%;
31.7%;
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                                                                                                                                                 from GB/EMBL/DDBJ
                                                                                                                                                                                                               October 1996
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#text_change 15-Oct-1999

492

273

435

375

DB 2; 108;

Length 503; Indels

49;

Gaps

8

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RESULT 10
JC6507
caspase-2 - rat
C;Species: Rattus
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A;Residues: 1-435 <WANN>
A;Cross-references: GB:Ul3021; NID:g537291;
C;Keywords: alternative splicing; apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Ich-1, an Ice/ced-3-related gene, A; Reference number: A54821; MUID:94373811; A; Accession: A54821
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Best Local :
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Best Local
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                                                                                                                                                                                                                          IVALLSHGVEGAIYGVDGKLLQLQEVFQLFDNANCPSLQNKPKMFFIQACRGDETDRGVD
                                                                                                 LAQVFSERACDMHVADMLVKVNALI-KDREGYAPGTEFHRCKEMSEYCSTLCRHLYLF
                                                                                                                               LCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFY
                                                                                                                                                              QQDGKNHAGSPGCEESDAG-KEKLPKMRLPTRSDMICGYACLKGTAAMRNTKRGSWYIEA
                                                                                                                                                                                                                                                         VCVLLSHGEEGIIFGTNGP-VDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGI- 172
                                                                                                                                                                                                                                                                                       TGEKELEFRSGGDVDHSTLYTLFKLLGYDVHVLCDQTAQEMQEKLQNFAQLPAHRVTDSC
                                                                                                                                                                                                                                                                                                                  HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSK-EDHSKRSSF
                                                                                                                                                                                                                                                                                                                                                                                  ENTENSVDSK-----SIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WFIQSLCAMLKQYADKLEFMHILTRVNRKVA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRDFAKHE-SHGDSAILVILSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFIQAVCEVFSTHAKDMDVVELLTEVNKKVA 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPAFLRRGWDNRDGPLFNFLGCVRPQVQQVWRKKPSQADILIAYATTAQYVSWRNSARGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEENVIIGVDDIPISTHEIYDLLNAANAPRLANKPKIVFVQACRGERRDNGFPVLDSVDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93/2;
        norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178/1;
                                                                                                                                                                              -ETDSGVDDDMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.18;
32.18;
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27.9%;
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        (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288/3; 360/1; 402/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 328.5; DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 352; DB 2;
Pred. No. 6.4e-21;
        rat)
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID: g537292
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                   120;
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YEMNSNPRGTVLILSNENF - - - KNMERRVGTKQDEVNLTKLFQKLQYTVICKRNLEAESM

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C;Accession. C;Accession of the cDNA A;Title: Cloning and expression of the cDNA Expression of the cDN
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                                                                                                                                                                                                   A; Description:
C; Keywords: cys
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A; Residues: 269-536 <
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A; Residues: 1-536 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T43633
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 273, 35109-35117, 1998
A; Title: Identification of multiple Caenorhabditis elegans
A; Reference number: Z22587; MUID:99074291; PMID:9857046
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C;Accession: T43633; T43636
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                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T43636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references:
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A; Residues: 1-452 <SAT>
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                                                                                                        Query Match
Best Local :
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                                                                                                                                                                                                                                                                     Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Matcr
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 KPKLFIIQACRGTELDCGI---
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YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVELMRDVSK-EDHSKRSSFVCVLLSHGEEGIIFGTNGP-VDLKKITNFFRGDRCRSLTG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                          EMBL: AF088286;
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                                                                                                                                                                                                                                                                                                                                                                                                                              <SH2>
                                                                                                     21.2%; 29.5%;
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                                                                    Score 310.5; DB 2;
Pred. No. 1.7e-17;
2; Mismatches 91;
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                                                                                                                                                                                                                                                                                                                                                                                       NID:g4063369; PIDN:AAC98293.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID: 94063367; PIDN: AAC98292.1;
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PMID:9427555
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                                                                                                                                                                                                                             processes
                                                                                                                                                                                                                                                                                                                                                                                       PID: 94063370
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                                                                 Gaps
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RESULT 13
T27021
hypothetical protein Y48E1B.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Contains: caspase 2B
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: csp-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AF088289; NID:g4063375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 564-826 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross·references:
A;Accession: T43639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-826 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Identification of multiple Caenorhabditis elegans A; Reference number: Z22587; MUID:99074291; PMID:9857046 A; Accession: T43638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: T43638; T43639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caspase-related proteinase 2A (EC 3.4.22.-) - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                 KYEA
                                                                                                                                                              EFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                                                              TSSSQADLLVSFSTSPGFLSFRDETKGTWYIQELYRVIIENAKDTHLADLLMETNRRVVE 797
                                                                                                                                                                                                                               ---VEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVAT 245
                                                                                                                                                                                                                                                                                                                                                                        YEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNG-PVDLKKITN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                          ESMDSGISLDNSYKMDYPEMGLC--IIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLK 82
                                                                                                                                                                                                                                                                                                     FFRGDRC-RSLTGKPKLFIIQACRGTELDCGIETDSGVDD------DMACHKIP---
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                                                                                                                                                                                                                                                                                                                                        YQSTSYDNLKSSEILETVRQFTQSNHG--DSLIITIMSHGDQGLLYGVDGVPVQMLDIID
                                                                                                                                                                                                                                                                                                                                                                                                             EDASDGKKIDETRKYRNNRSSKCRAIIINNVVF---CGMEKRIGSDKDKKKLSKLFERLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STTDGFTSYRDEEAGTWYIKSMCKVFNKHSKTMHLLDILTETGRNVVTKYENVQGNVVL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEAIKEFAEMAHT--DSIILFLLSHGDGAGSVFGIDDMPVNVMEVSTYLAYH--QNLLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273, 35109-35117, 1998
                                                                                                                                                                                                                                                                  -CTASLAKKPKWLMCVCCRGDRIDRAVRCDGFIDNFFDRFPKFFQFMKSKFPSHQ
                                                                                                                             -DKVVIVCKQAPEFWSRFTKQLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: AF088288; NID: g4063373; PIDN: AAC98295.1;
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Pred. No. 6.2e-17;
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15-Oct-1999 #text_change
                                                                                                                             824
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 15-Oct-1999
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A; Introns: 9/3; 59/3; 135/1;
C; Keywords: differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 277, 655-659, 2000
A;Title: Caspase-14: Analysis of gene structure and mRNA expression
A;Reference number: JC7517; MUID:20517231; PMID:11062009
                                                                                                                                                                                                                                                                                                                                                                  C; Comment:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-242 <ECK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Homo sapiens (man)
C; Date: 30-Jun-2001 #sequence
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JC7517
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                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AF097874
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Contents: Epidermal keratinocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Eckhart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: JC7517
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A; Introns: 79/3;
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A;Experimental source: clone Y48E1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-642 <WIL>
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R; McMurray,
                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                         Query Match
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     117
                                     148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208
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                                                                                                                                                                                                                                      Local
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                      CRSLTGKPKLFIIQACRGTELDCGIETDSGVDDDMAC----HKIPVEADFLYAYSTAPGY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VELMRDVSKEDHSKRSSFVCVLLSHGE-EGIIFGTNG-PVDLKKITNFFRGDRCRSLTGK 154
CQALRAKPKVYIIQACRGEQRDPG-ETVGGDEIVMVIKDSPQTIPTYTDALHVYSTVEGY 175
                                                                                                                                                                            DNSYKMDYPEMGLCIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93
                                                                     EQFQEELEKFQQAIDSREDPVSCAFVVLMAHGREGFLKGEDG--EMVKLENLFEALNNKN 116
                                                                                                       EEIVELMRDVSKEDHSKRSSFVC---VLLSHGEEGIIFGTNGPVDLKKITNFF---RGDR 147
                                                                                                                                          EEKYDMSGARLALILCVTK------AREGSEEDLDALEHMFRQLRFESTMKRDPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKLFIIQACRGTELDC-----GIETDSGVDDDMACHKIPVEADFLYAYSTAPGYYSWR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEAIKEFAEMAHT--DSIILFLLSHGDGAGSVFGIDDMPVNVMEVSTYLAYH--QNLLLK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEMNSNPRGTVLILSNENF---KNMERRVGTKQDEVNLTKLFQKLQYTVICKRNLEAESM 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKWVAVSACRGGEIDLIFFAFQPGTFTS---
                                                                                                                                                                                                                                                                                                                                                                               This enzyme accumulates during keratinocyte differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L.; Ban,
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                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122/3; 239/2; 286/3; 333/1; 417/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.; Fischer, H.; Tschachler, 1 es. Commun. 277, 655-659, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
                                                                                                                                                                                                                                    18.8%;
31.9%;
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                                                                                                                                                                                                                                                                                                           174/1;
                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Mismatches
                                                                                                                                                                                                                 Score 274.5;
Pred. No. 5.3e
39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:CAB07698.1; GSPDB:GN00020; CESP:Y48E1B.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 277; DB 2;
Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                           208/3
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                                                                                                                                                                                                                                    .3e-15;
                                                                                                                                                                                                                                                   DB 2;
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96	
73	Qy 215 FIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKOIPCIVSM-LTKEL 273
14	Qy 166 TELDCGIETDSGVDDDMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSW 21 : : : : :
.65	OY 112 SSFVCVLLSHG-EEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRG 165
11 26	QY 53 KNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSK-EDHSKR 111
69	Qy 6 NSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPENGLCIIINN 52
3 11;	Query Match 16.9%; Score 247.5; DB 2; Length 402; Best Local Similarity 29.0%; Pred. No. 1.6e-12; Matches 88; Conservative 46; Mismatches 124; Indels 45; Gaps
18	Status: preliminary Molecule type: DNA Molecule type: DNA Residues: 'MAV',7-402 <res> Cross-references: EMBL:U04269; NID:g476217; PIDN:AAA56992.1; PID:g4762 Genetics:</res>
ne encoding into	The structure and complete nucleotide sequence of the murine genee number: A54264; MUID:94307735; PMID:8034321
	A; Note: sequence extracted from NCBI backbone (NCBIP:126931) R;Casano, F.J.; Rolando, A.M.; Mudgett, J.S.; Molineaux, S.M. Genomics 20, 474-481, 1994
	A: Molecule type: mRNA A: Residues: 1.187,189-402 <mol> A: Fyperimontal source: macrophago</mol>
	Accession: A4, Status: prelin
requires a str	Proc. Natl. Acad. Sci. U.S.A. 90, 1809-1813, 1993 A;Title: Interleukin 1 beta (IL-1 beta) processing in murine macrophages A;Reference number: A47258; MUID:93189587; PMID:8446594
G.; Chin, J.;	Motte: sequence extracted from NCBI backbone (NCBIP:117473) Molineaux, S.M.; Casano, F.J.; Rolando, A.M.; Peterson, E.P.; Limjuc
)lecule type: nucleic acid saidues: 1-402 <net></net>
	cession: A46495
Α.	itle: Mole eference n
Jenkins, N.A.;	<pre>itt, M.A.; Cerretti, D.P.; Berson, D.R.; Seavitt, J.; Gilbert, D.J.; Immunol. 149, 3254-3259, 1992.</pre>
2000	se) sion 18-Nov-1994 #text_change 01-Dec-
	JLT 15 195 1 beta conve
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	264 CIVENITREIV 274
229	:: : : : :
263	Qy 204 YSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIP 2

Qy 274 YFY 276 | : Db 397 YLF 399

Search completed: December 2, 2002, 12:57:09 Job time: 17.2828 secs

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Result
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                                                             h caspase-8
homo sapien
caenorhabdi
caenorhabdi
gallus gali
gallus gali
homo sapien
rattus norv
bos taurus
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4 mus musculu
4 mesocricetu
0 homo sapien
8 mus musculu
2 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drosophila
spodoptera
drosophila
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æ	90.5	92.5	93	96	183	202	213.5	217.5	222.5	232.5	234.5
ь. С	5 . 2	6.3	6.4	6.6	12.5	13.8	14.6	14.9	15.2	15.9	16.0
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P06241 homo sapien	P39688 mus musculu	068006 b bacitraci	Q05876 qallus qall	P27446 xiphophorus	015519 h casp8 and	035732 m casp8 and	Q9n2il sus scrofa	P70343 mus muscul	P29466 homo sapien	P51878 homo sapie	Q9mzv7 canis fami

ALIGNMENTS

RA	R R R	R R A	RX RA	RP	RL	RT	RA RA	RA A	RX	o R	RE	g R	RT.	RA A	RX	R X	R.	RT	RT	RA	R 2	RP	RN	28	8 8	GN GN	멅		DI.	33	AC L	RES
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277. MEDLINE-97197830; PubMed-9045680; Mittl P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,	519-625(1996).	rM., Peterson E.P., Rasper D.M., Ruel R., Vaillancourt J.P. rry N.A., Becker J.W.; Rasper D.M., Ruel R., Vaillancourt J.P. ree-dimensional structure of anomaln/CDD32 a Year modiator	, Gallant N	(4) X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277	Nature 376:37-43(1995).	Ification and inhi	Smulson M.E., Yamin TT., Li V.L.,	Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K., Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik v A	0r 29-40 AND 1/3-193, AND FUNCT 95319529; PubMed=7596430;	175 103 115	Cell 81:801-809(1995).	t cleaves the death substrate poly(ADP-ribose).	"Yama/CPP32 beta, a mammalian homolog of CED-3, is a Crma-inhibitable	T., O'Rourke K., Desnoyers S., Zeng	MEDLINE=95292347; PubMed=7774019;	SEQUENCE FROM N.A.	J. Biol. Chem. 269:30761-30764(1994).	caenormaburcis eregans cerr dearn protein ced-3 and mammarian interleukin-1 beta-converting enzyme.":	l human apoptotic protein with hom	Fernandes-Alnemri T., Litwack G., Alnemri E.S.;	T1550E=T-CELL; MEDLINE=95074098; PubMed=7983002;	SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).		utheria; Primates; Catarrhini; Hominidae; Homo.		CPP32.		precursor (EC 3.4.22) (Cysteine protease CPP32)	15-JUN-2002 (Rel. 41, Last annotation update)		CE3_HUMAN ST/ 42574;	

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AGOIDMET Y.P., NICHOLSON D.W., RASPET D.M., KAICHMAN M.A., KOIDMEN AGOIDMEN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

Lev D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A., Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S., Levy M.A., DeWolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S., Ryan M.D., Haltiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.C., Johanson K., Concha N.O., Chan W., Abdel-Mequid S.S., Badger A.M., Johanson K., Concha N.O., Suva L.J., Gowen M., Nuttall M.E.;

"Potent and selective nonpeptide inhibitors of caspases 3 and 7 Inhibit apoptosis and maintain cell functionality.";

J. Biol. Chem. 275:16007-16014(2000).
                                                                                                                                                                              EMBL;
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Genew; HGNC:1504; CASP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96353838; .PubMed=8755496;
Fernandes-Alnemri T., Armstrong R.C., Krebs J.,
Wang L., Bullrich F., Fritz L.C., Trapani J.A.,
Litwack G., Alnemri E.S.;
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                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is ified and this statement is not removed. Usage by and fo ities requires a license agreement (See http://www.isb-sib.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LI AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND I IN TESTIS. ALSO FOUND IN MANY CELL LINES, HIGHEST EXPRESSION IN CELLS OF THE IMMUNE SYSTEM.

PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10 GENERATES THE TWO ACTIVE SUBMITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUN OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUPAND VICE VERSA
                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS
                                                1CP3;
                                                                                                U13737; AAA65015.1; -. U13738; AAB60355.1; -. U26943; AAA74929.1; -. 1PAU; 07-JUL-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VICE VERSA
                          14.003;
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ct.";
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                                                                                                                                                                                                                                                                                                                                                          collaboration -
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ICE3_RAT
ID ICE3
AC PISS
AC O1-C
DT 01-C
DT 01-C
DT 15-C
DE Apoul
DE (SC)
GN CASI
ON RAT
OC Euka
OC Mam
OX NCB
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Best Local
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InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                               ICE3_RAT STANDARD; PRT; 277 AA.
P55213; P70543; Q62993; P97699;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP Cleavage activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
CHAIN
ACT_SITE
ACT_SITE
                                            Fletcher F.A.
                                                                 SEQUENCE FROM N.A. MEDLINE=96358624; PubMed=8761296;
                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                     Molecular characterization cysteine protease resembli
                                                       Juan T.S.-C., McNiece
                                                                                                 NCBI_TaxID=10116;
                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                              CASP3 OR CPP32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01122; CASPASE_CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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            cysteine protease
nd CED-3.";
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                                                                                                                                                                                                                                                                                                    RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                                                                                                                                                                                                                                                                MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                         MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                                                                                                                                                                                                                                                                                                              HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                                        (LICE)
 13:749-755(1996)
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                                                                                                           Chordata;
Rodentia;
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                                                       I.K.,
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                    of mouse and rating interleukin-1
                                                       Jenkins
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APOPAIN P12 SU
BY SIMILARITY.
BY SIMILARITY.
D. -> E (IN ISO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1460;
Pred. No. 1
                                                                                                          Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                       N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.7e-115;
                                                                                                                      Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 SUBUNIT.
2 SUBUNIT.
                                                     Gilbert
                                                                                                                                                                                                                                                                                         277
                                                                                                           Muridae;
                     beta
                                CPP32 beta gene
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                                                     D.J.,
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                    converting
                                                                                                                       Euteleostomi;
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                                                     Copeland
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                    enzyme
                                 encoding
                                                                                                           Rattus.
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SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS;
PROSITE; PS01121; CASPASE_HIS;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWI
between
                                                                                               Pfam; Processians 
                                                                                                                                                              InterPro; IPR002398; ICE_D10.
InterPro; IPR002138; ICE_D10.
InterPro; IPR001309; ICE_D20.
Pfam; PF00655; ICE_D10; 1.
Pfam; PF00656; ICE_D20; 1.
                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT PROTECUTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREEPS) BETWEEN THE BASIC HELIX-LOOPHELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.

CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).

-i- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                             MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K., Rosteck P. Jr., Polifier G.G., Paul S.M., Polifier G.G., Paul S.M., Polifier G.G., Paul S.M., Interleukin-lbeta-converting enzyme (ICE)-related protease (IRP) and its possible role in apoptosis of cultured cerebellar granule neurons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I., Hirshfield A.N., Tilly J.L.;
"Interleukin-1 beta-converting enzyme-related proteases (IRPs) and mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa cells of the ovarian follicle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
MEDLINE-97184204; PubMed-9030616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takovlev A.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-264 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              optosis of cultured cerebellar Neurosci. 17:1561-1569(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).

(BY SIMILARITY).

SUBCELLULAR LOCATION: Cytoplasmic.

TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE BUT NOT IN KIDNEY OR TESTIS.

DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED REGIONS OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VICE VERSA (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR A
                                                                                                                                                                                                                                                                                                                                 ; U58656;
; P42574;
                                                                                                                                                                                                                                                                                                                                                  U49930; AAC52765.1; -. U34685; AAC52261.1; -. U84410; AAB41792.1; -. U58656; AAB02722.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the Ex-
European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                           C14.003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLEAVAGE BY GRANZYME
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                                                                                                                                       IL1BCENZYME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
CPP32 during apoptosis.";
EMBO J. 15:1012-1020(1996).

-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS
PROTEDLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
216-ASP-[-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
                                                             Wang X., Zelenski N.G., rang u. Goldstein J.L.;
"Cleavage of sterol regulatory
                                                                                                                                                                                                                                                                          ICE3_CRILO
Q60431;
                                                                                                                                                                Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                 _CRILO
                                                                                                      MEDLINE=96183185;
                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                  CASP3 OR CPP32.
                                                                                                                                                                                                                      Apopain precursor protein) (CPP-32)
                                                                                                                                                                                                                                          01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                       RKVATEFESFSLDATFHAKKQIPCIVSMLTKELYFYH
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35, Last sequence 41, Last annotations
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41, Last annotation update)
(EC 3.4.22.-) (Cysteine protease CPP32) (Yama (Caspase-3) (CASP-3) (SREBP cleavage activity
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                                                                                                     PubMed=8605870;
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                                                                                         J.,
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T -> 2
H -> 1
F -> 2
T -> 2
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Pred. No. 1.8e-103;
3; Mismatches 17;
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BY SIMILARITY.
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> S (IN REF. 2).
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> V (IN REF. 2).
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> G (IN REF. 3).
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InterPro; IPR002138; ICE_D10.
InterPro; IPR001399; ICE_D20.
Pfam; PF00655; ICE_D10; 1.
Pfam; PF00656; ICE_D20; 1.
Pfam; PF00656; ICE_D20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
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PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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HSSP; P42574;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPERTIDES LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODINERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR VICE VERSA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).

SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUN
                                                                 RKVATEFESFSLDSTFHAKKQIPCIVSMLTKELYFYH
                                                                              RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                                                               DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                                                                                                                                                                                          MTPRSGTDVDAAKLRETFMALKYEVRNKNDLTREEIVELMKNASKEDHSKRSSFVCVILS
                                                                                                                                                                                                                                                                               MENNETSVDSKSIKNFEVKTIHGSKSMDSGIYLDSSYKMDYPEMGVCIIINNKNFHKSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                  HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                                                                                                                         MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
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                                                                                                                                                                                                                                                                                                                                                       Similarity
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176
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                                                                                                                                                                                                                                                                                                                                                                                                      ol protease; Zymogen; Apoptosis.

1 9 BY SIMILARITY.

0 28 BY SIMILARITY.

10 28 BY SIMILARITY.

11 175 APOPAIN P17 SUBUNIT.

12 BY SIMILARITY.

13 163 BY SIMILARITY.
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  STANDARD;
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87.0%;
                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                  Score 1293;
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 PRT;
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 277
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Fernandes Alnemri T., Litwack G., Alnemri E.S.;

Submitted (MAY-1997) to the EMBL/GenBank/DBBJ databases.

11 FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES

RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT PROTEDLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217 BOND. CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 215-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX'LOOP-HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN. CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).

CLEAVES AND ACTIVATES CASPASE-6, -7 AND AN ALA, RELEASING THE MATURE CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.

-1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P70677; 008668;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                        ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97190206; PubMed=9038361; van de Craen M., Vandenabeele P., van Loo G., Molemans F., Schotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.; "Specific expression of CPP32 in sensory neurons of mouse embry activation of CPP32 in the apoptosis induced by a withdrawal of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a cysteine
and CED-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-96338624; PubMed-8761296;
Juan T.S.-C., McNiece I.K., Jenki.
Fletcher F.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apopain precursor protein) (CPP-32) (SCA-1) (LICE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of seven murine FEBS Lett. 403:61-69(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fiers W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGF."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncogene 13:749-755(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                            PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERAY TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTI LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CP932 ALSO OCC VICE VERSA (BY SIMILARITY).
                                                                                                                                                                                                                         (BY SIMILARILL).
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN, LUNG
                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR CPP32
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(hordata;
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35, Last sequence update)
41, Last annotation update)
(EC 3.4.22.-) (Cysteine protease CPP32) (Yama (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
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Sciurognathi; Muridae;
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interleukin-1
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P., van Criekinge W., Beyaert
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beta converting
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Best Local
                                         ICE3_XENLA STANDARD P55866; 01-NOV-1997 (Rel. 35, C 01-NOV-1997 (Rel. 35, L 15-JUN-2002 (Rel. 41, L Apopain precursor (EC 3 (CASP-3) (XCPP32).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:107739; Casp3.
InterPro; IPR002398; ICE_P10.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
Pfam; PF00655; ICE_P10; 1.
Pfam; PF00655; ICE_P20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                    _XENLA
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CONFLICT
CONFLICT
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ACT_SITE
ACT_SITE
CONFLICT
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EMBL; D86352;
EMBL; Y13086;
EMBL; U19522;
HSSP; P42574;
                                 CASP3
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SEQUENCE
             Xenopus
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PROPEP
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PROSITE: PS01121; CASPASE_HIS; 1.
PROSITE: PS50207; CASPASE_P10; 1.
PROSITE: PS50208; CASPASE_P20; 1.
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                                                                                                                                                                                                                                                           RKVATEFESFSLDSTFHAKKQIPCIVSMLTKELYFYH
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CAA73528.1;
AAC53196.1;
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                                                           protease CPP32) (Caspase-3)
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Query Match
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Matches 156
 CHAIN
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SEQUENCE
 CHAIN
 between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contenmodified and this statement is not removed. Usage by entities requires a license agreement (See http://www.is
 PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
 Pfam; PF00655; ICE_p10; Pfam; PF00656; ICE_p20;
 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 -I- FUNCTION: IMPORTANT MEDIATOR OF APOPTOSIS. AT THE ONSET OF APOPTOSIS IT PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217 BOND (BY SIMILARITY).
-!- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNITS.
 "Induction of apoptosis and CPP32 myoblastic cell line derived from J. Biol. Chem. 272:5122-5127(1997)
 EMBL; D89784; BAA14018.1; -. HSSP; P42574; 1PAU.
 PROPEP
 Hydrolase;
 MEROPS; C14.003;
 OTHER CASPASES (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 -
 180
 InterPro;
 InterPro;
 InterPro;
 Yaoita Y.,
 MEDLINE=97184166;
 SEQUENCE FROM N.A.
 Amphibia; Batrachia;
Xenopodinae; Xenopus
 Eukaryota;
 229
 169
 120
 110
 61
 50
 سو
 SUBCELLULAR LOCATION: Cytoplasmic (By similarity) MISCELLANEOUS: THE SUBUNITS ARE DERIVED FROM THE SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM AN OTHER CASPASES (BY SIMILARITY).
KLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFY
 DSGIETDSCSEPREEIQRIPVEADFLYAYSTVPGYCSWRDKMDGSWFIQSLCKMIKLYGS
 DCGIETDSGVDDDMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYAD
 KRSSFVCVLLSHGEE-GIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTEL
 INNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHS
 KRSSFVCAILSHGEEDGSICGVDVPIHIKNLTDLFRGDRCKTLVGKPKIFFIQACRGTEL
 INNKNFH-SSNMAVRNGTDVDALKLHETFTGLGYEVMVCNDQKSSDIIGRLKKISEEDHS
 MEESQNGVKYGGDATDAKEYFTIQPRSLQNCDLKDIERKTKFAHLQNYRTNYPEMGMCLI
 MENTENSV-----DSKSIKNLEPKIIHGSESMD----SGISLDNSYKMDYPEMGLCII 49
 SWISS-PROT entry is copyright. It is produced through
 Similarity
 IPR002138; ICE_p10
IPR001309; ICE_p20
 IPR002398;
 Nakajima K.;
 Metazoa; Chordata; Craniata; Vertebrata;
 282
 Conservative
 AA;
 protease;
 PubMed=9030578;
 32124 MW;
 53.8%;
 Anura; Mesobatrachia; Pipoidea; Pipidae;
 Zymogén; Apopto:
BY SIMILARITY
 40;
 Score 786.5;
Pred. No. 6.1e
40; Mismatches
 BY SIMILARITY
BY SIMILARITY
 APOPAIN P17 SUBUNIT APOPAIN P12 SUBUNIT
 CPP32 expression by thyroid from tadpole tail.";
 CB390E6980CAB77F CRC64;
 Apoptosis
 There are no rest
 .1e-59;
 DΒ
 73;
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 Length
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 Euteleostomi;
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 PROBABLY
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 EMBL outstation
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 282;
 19;
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 collaboration - L outstation
 Gaps
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 168
 109
 239
 119
 60
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RESULT
ICE7_M
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 Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPPOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS). OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).
-I- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
-I- SUBCELLULAR LOCATION: Cytoplasmic.
-I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
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 This
 FEBS Lett.
 van de Craen M., Vandenabeele P.,
 MEDLINE=97190206; PubMed=9038361;
 differentiation
 MEDLINE-97224489; PubMed-9070923;
Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A.,
Copeland N.G., Fletcher F.A.;
 SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine
 SEQUENCE FROM N.A.
 "Characterization of seven murine caspase family members."; FEBS Lett. 403:61-69(1997).
 Fiers W.
 van Loo G., Molemans
 SEQUENCE FROM N.A.
 Mukasa
 SEQUENCE FROM N.A.
 Genomics
 "Identification and mapping of Casp7, a CPP32 beta, interleukin-1 beta convertin
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
 protease Mch-3).
CASP7 OR MCH3 OR LICE2.
 Biochem. Biophys.
 "Wortmannin enhances CPP32-like activity differentiation of P19 embryonal carcinon
 MEDLINE=97236307; PubMed=9125129;
 Mus musculus (Mouse)
 P97864;
 240
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 EXPRESSION IN THE BRAIN.

PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE SUBURITS. PROPERTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBURIT OF CASPASE-7 AND THE LARGE SUBURIT OF CPP32 PROTEASE ALSO OCCUR AND VICE VERSA (BY SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 MOUSE
 HLELIQILTCVNHMVALDFE--
 008669;
 40:86-93(1997).
 Khoroku
 STANDARD;
 Res.
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 .
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 Commun.
 Tsukahara
 embryonal carcinoma
 Schotte
 Craniata; Vertebrata; |
Sciurognathi; Muridae;
 PRT;
 232:192-197(1997).
 Casp7, a cysteine converting enzyme,
 TFHAKKQIPCVVSMLTKSFYFF
 Ρ.,
 T.,
 Declercq W., van
P., van Criekinge
 Momoi M.Y., Kimura
 303
 (See http://www.isb-sib.ch/announce/
 during
 as its content
 cells induced
 Usage
 neuronal
 protease resembling
, and CED-3.";
 protease) (Apoptotic
 Σ.
 den Brande
 Euteleostomi;
; Murinae; Mus.
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 P55214;
01-OCT-1996;
01-OCT-1996;
15-JUN-2002
 _MESAU
 EMBL; U67321; I
EMBL; D86353; E
EMBL; Y13088; C
 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-7 precursor (EC 3.4.22.) (ICE-like apoptotic protease
(ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity
 Mesocricetus auratus (Golden hamster).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 ACT_SITE
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
 PROPEP
CHAIN
ACT_SITE
SEQUENCE FROM N.A.,
 Mesocricetus.
NCBI_TaxID=10036;
 CASP7 OR MCH3.
 PRINTS; PRO0376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
 ICE7_MESAU
 Pfam; PF00655; ICE_p10; 1. Pfam; PF00656; ICE_p20; 1.
 MGD; MGI:109383; Casp7.
InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10
InterPro; IPR001309; ICE_p20
 CHAIN
 PROPEP
 Hydrolase;
 MEROPS;
 HSSP; P42574;
 EMBL; BC005428;
 300
 274
 240
 180
 157
 120
 97
 60
 37 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
 ΥF
 YF 275
 WFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKEL
 LFIIQACRGTELDCGIETDSGVDDDMAC---HKIPVEADFLYAYSTAPGYYSWRNSKDGS
 WFVQALCSILNEHGKDLEIMQILTRVNDRVARHFESQSDDPRFNEKKQIPCMVSMLTKEL
 VELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPK 156
 YRMDFQKMGKCIIINNKNFDKATGMDVRNGTDKDAGALFKCFQNLGFEVTVHNDCSCAKM 119
 QDLLRKASEEDHSNSACFACVLLSHGEEDLIYGKDGVTPIKDLTAHFRGDRCKTLLEKPK
 LFFIQACRGTELDDGIQADSGPINDIDANPRNKIPVEADFLFAYSTVPGYYSWRNPGKGS
 144;
 301
 Similarity
 C14.004; -
 303
 Thiol
 Conservative
 48
 CAA73530
 1PAU.
 BAA19730.1;
 AAC53068.1; ALT_INIT.
 AA;
 STANDARD;
 AAH05428.1;
 protease;
 186
11
45
49
 AND PARTIAL SEQUENCE
 34060 MW;
 51.2%;
59.5%;
 BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

CASPASE-7 SUBUNIT FOR SIMILARITY.

BY SIMILARITY.
 36;
 Score 748.5; I
Pred. No. 1e-5
36; Mismatches
 BY SIMILARITY.
BY SIMILARITY.
EL -> DW (IN REF.
 VR.
 . , ,
 -> T (IN REF. 2).
R -> RQ (IN REF. 2).
747787B5BDE5F744 CRC64;
 No. 1e-55;
 303
 SUBUNIT P20
 A
 DB 1;
 59;
 P11
 2).
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Matches 141;
 Query Match
 InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
Pfam; PF00655; ICE_p20; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01121; CASPASE_CYS; 1
PR0SITE; PS01121; CASPASE_HIS; 1
PR0SITE; PS050207; CASPASE_P10; 1
PR0SITE; PS50208; CASPASE_P20; 1
PR0SITE; PS50208; CASPASE_P20; 1
 CHAIN
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ACT_SITE
 SEQUENCE
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 PROPEP
 Hydrolase;
PROPEP
 240
 InterPro;
 MEROPS; C14.004;
 EMBL;
 or send
 Pai J.-T., Brown M.S., Goldstein J.L.; "Purification and cDNA cloning of a second protease that cleaves and activates sterol
 214
 157
 180
 120
 Proc
 proteins.";
 MEDLINE-96224303; PubMe
Pai J.-T., Brown M.S.,
 STRAIN-Syrian;
 97
 60
 37
 Local Similarity
 (BY SIMILARITY).

SUBCELLULAR LOCATION: Cytoplasmic.

SUBCELLULAR LOCATION: Cytoplasmic.

SUBCELLULAR LOCATION: Cytoplasmic.

PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE SUBUNITS. PROPERTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND CASPASE-7.
 VICE VERSA (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
 BOND. OVEREXPRESSION PROMO
SIMILARITY).
SUBUNIT: HETERODIMER OF A
(BY SIMILARITY).
 FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION: CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|-GLY-217 BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY
WFVQALCSILDEHGKDLEIMQILTRVNDRVARHFESQCDDPCFNEKKQIPCMVSMLTKEL
 WFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKEL
 LFIIQACRGTELDCGIETDSG----VDDDMACHKIPVEADFLYAYSTAPGYYSWRNSKDGS
 QDLLRKASEEDHSNSACFACVLLSHGEENLIYGKDGVTPIKDLTAHFRGDRCKTLLEKPK
 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
 LFFIQACRGTELDDGVQADSGPINETDANPRYKIPVEADFLFAYSTVPGYYSWRNPGKGS
 YRMDFEKMGKCIIINNKNFDKVTGMDVRNGTDKDAEALFKCFRSLGFDVVVYNDCSCAKM
 P42574;
 U47332; AAC52595.1; -.
 an email to license@isb-sib.ch).
 IPR002398;
 Thiol
 186
303 AA;
 24
199
207
144
 Conservative
 1PAU.
 TISSUE=Liver;
 protease;
 PubMed=8643593;
 198
198
206
303
 34037 MW;
 58
58
 .38;
 35;
 Zymogen;
 Score
Pred.
 BY
BY
 CASPASE-7 SUBUNIT
BY SIMILARITY
CASPASE-7 SUBUNIT
 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT
 EA29356D90984648 CRC64;
 SIMILARITY.
 Mismatches
 726.5;
No. 7.3
 Apoptosis.
 .3e-54;
 DB 1;
 apoptosis-related cysteine regulatory element binding
 C14.
 P11
 Length
 Indels
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 Gaps
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 179
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 213
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RESULT 8
ICE7_HUMAN
 ICE7_HUMAN STANGED TO THE PROPERTY OF THE PROP
 apoptotic cysteine protease containing two FADD-like Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CRESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND
 Fernandes-Alnemri T., Armstrong R. Wang L., Bullrich F., Fritz L.C., Litwack G., Alnemri E.S.,
 Juan T.S.-C., McNiece I.K., Argento J.M.,
Copeland N.G., Fletcher F.A.;
 Strausberg
 "Identification and mapping of Casp7, a cy CPP32 beta, interleukin-1 beta converting
 TISSUE-Fetal lung, and Fetal spleen; MEDLINE-97224489; PubMed-9070923;
 (ILL CASP7 OR MCH3.

CASP7 OR MCH3.

Homo sapiens (Human).

Horota; Metazoa; Chordata;

horia; Primates;
 Submitted
 TISSUE-Skin;
 SEQUENCE FROM
 CPP32
 Fernandes-Alnemri T., Takahashi A., Æ
Fritz L.C., Tomaselli K.J., Wang L.,
Earnshaw W.C., Litwack G., Alnemri E.
 Lippke J.A., Gu Y., Sarnecki C., Caro "Identification and characterization cysteine protease similar to CPP32.", J. Biol. Chem. 271:1825-1828(1996).
 'In vitro activation of CPP32 and Mch3 by Mch4,
 MEDLINE=96353838;
 PROCESSING
 SEQUENCE FROM N.A. (ALPHA AND ALPHA'
 TISSUE=T-cel
 MEDLINE=96147144;
 "Mch3, a novel human apoptotic cysteine
CPP32.";
 MEDLINE=96105019; PubMed=8521391;
 SEQUENCE FROM N.A. (ALPHA AND BETA
 TISSUE-Spleen;
 SEQUENCE
 cell
 "ICE-LAP3, a novel mammalian homologue
 Dixit V.M.;
 Duan
 SEQUENCE FROM N.A. (ALPHA ISOFORM). MEDLINE-96139498; PubMed-8576161;
 cell death protein Ced-3 factor-induced apoptosis
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 Biol.
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 40:86-93(1997).
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 Chinnaiyan
 Chem.
 (OCT-2001)
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 55:6045-6052(1995).
 N.A.
 N.A. (ALPHA ISOFORM).
 apoptosis.";
271:1621-1625(1996)
 PubMed=8755496;
 PubMed=8567622;
 (ALPHA ISOFORM
 A.M., Hudson P.L.,
 ç
 Takahashi A., Armstrong R.C., Krebs K.J., Wang L., Yu Z., Croce C.M., Sa
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 is activated
 EMBL/GenBank/DDBJ databases
 Craniata; Vo
Catarrhini;
 Caron
 .C., Krebs J.,
Trapani J.A.,
 ISOFORMS).
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 a cysteine protease resembling ting enzyme, and CED-3.";
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 of the Caenorhabditis
 Wing J.P.,
 protease highly related
 CPP32/Mch2
 Vertebrata;
 Jenkins
 Hominidae;
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 Srinivasula S.M
Tomaselli K.J.,
 OF CASPASES
AND ACTIVATES
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PROTEOLYTICALLY
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Query Match
 EMBL; U39613; AAC50346.1; --
EMBL; U40281; AAC50352.1; --
EMBL; U37448; AAC50303.1; --
EMBL; U37449; AAC50304.1; --
EMBL; U67319; AAC51152.1; --
EMBL; U67320; AAC51153.1; --
 CONFLICT
CONFLICT
SEQUENCE
 CHAIN
ACT_SITE
ACT_SITE
VARSPLIC
 CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-[-GLY-217 BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH.

-! ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.

-!- SUBUNIT: HETERODIMER OF A 20 KDa (P20) AND A 11 KDa (P11) SUBUNIT.

-!- SUBCELLULAR LOCATION: CYPOPLASMIC.

-!- ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING. THE BETA AND ALPHA'; ARE PRODUCED BY ALTERNATIVE SPLICING, THE BETA ISOFORM IS NOT PROTEDLYTICALLY ACTIVE.

-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE, LIVER, KINNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO EXPRESSION IN THE BRAIN.

-!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND VICE VERCA
 Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
 EMBL;
 MUTAGEN
 VARSPLIC
 PROSITE; PS01122; CASPASE_CYS;
PROSITE; PS01121; CASPASE_H1S;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
 PRINTS; PR00376; ILIBCENZYME. SMART; SM00115; CASC; 1.
 PROPEP
 InterPro;
 Genew; HGNC:1508; CASP7.
 EMBL;
 use by non-profit institutions as long as modified and this statement is not removed. \ensuremath{\mathbb{U}}
 '
 Hydrolase;
 MEROPS; C14.004;
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 tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
 SIMILARITY: BELONGS TO PEPTIDASE FAMILY CAUTION: WHAT WE CALL ALPHA' ISOFORM IS
 601761; -
 P42574;
 BC015799;
 FION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF.4 AS BETA IS ALREADY DEFINED IN REF.3 WE HAVE CALLED
 IPR002398;
IPR002138;
IPR001309;
 194
 24
199
207
144
186
 AAC51153.1; -.
AAF21460.1; -.
 A.
 1PAU.
 186
4
194
34276 ₁
 AAH15799.1;
 protease;
 303
 ICE_p10.
 49.6%;
 ICE_p20
 ¥.
 Zymogen;
 PSWRSTEKTWKSCRSSPG (IN ISOFORM C->A: NO APOPTOTIC ACTIVITY. D -> E (IN REF 5). G -> A (IN REF 1).
 (IN ISOFORM ALPHA').

VIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGT
ELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYY
SWRSPGROSWFVQALCSILEEHGKDLEIMGILTRVNDRYNA
HFESQSDDPHFHEKKQIPCVVSMLTKELYFSQ -> MESCS
VTQAGVQRRDLGRLQPPPPRLAEGPSLMMASRPTRGPSMTQ
MLILDTRSQWKLTSSSPIPRRQAITRGGAQEEAPGLCKPSA
 CASPASE-7
BY SIMILAR
 Score 725;
 -> E (IN REF. 5)
-> A (IN REF. 1)
CD373EE54A233CA4
 MDCVGWPPGRKWHLEKNTSCGGSSGICASYVTQM
 Apoptosis; Alternative splicing
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 Best Local Similarity 51.3
Matches 145; Conservative
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or send an email to ''-
 "Characterization (1997).
FEBS Lett. 403:61-69(1997).
-I- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
-I- FUNCTION: INVOLVED IN THE ACTIVATION. CLEAVES POLY(ADP-RIBOSE)
RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE)
POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES
PROCRAMMED CELL DEATH (BY SIMILARITY).
--- STRUNIT: HETERODIMER OF A 18 kDa. (P18) AND A 11 kDa (P11) SUBUNITIONAL PROCRAMMED CELL DEATH (BY SIMILARITY).
 This SWI
between
 EMBL; Y13087;
HSSP; P42574;
 -i- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GE
SUBUNITS (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 MEDLINE=97190206; PubMed=9038361; van de Craen M., Vandenabeele P., Devan Loo G., Molemans F., Schotte P.,
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
 MEROPS; C14.005;
 Fiers W.;
 STRAIN=C3H/An;
 SEQUENCE FROM N.A.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 008738;
 Mus musculus (Mouse).
 NCBI_TaxID=10090;
 ICE6_MOUSE
 259
 233
 199
 176
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 116
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 56
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 SUBCELLULAR LOCATION: Cytoplasmic TISSUE SPECIFICITY: HIGHLY EXPRESS
 TESTIS, AND
 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Event of Bioinformatics and the Bioinformatics
 MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
 CVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETD
 P42574;
 MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
 CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDGIQAD
 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV
 SGVDDDMAC----HKIPVEADFLYAYSTAPGYYSWRNSKDGSWEIQSLCAMLKQYADKLEF
 DKYTGMGYRNGTDKDAEALFKCFRSLGFDYIYYNDCSCAKMQDLLKKASEEDHTNAACFA
 ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF
 SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKDLEI
 EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF
 1PAU.
 CAA73529.1;
 STANDARD;
 HEART. LOWER LEVELS
 51.2%;
 49;
 Pred. No.
 PRT;
 EXPRESSED IN LUNG, LIVER, EVELS IN SPLEEN, SKELETAL
 Mismatches
 Declercq W., van P., van Criekinge
 (P18) AND A 11 kDa (P11) SUBUNIT
 276
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 Matches 104;
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 Srinivasula S.M., Fei
Armstrong R.C., Wang
Alnemri E.S.;
 TISSUE-Lymphocytes;
MEDLINE-97059171; PubMed-8900201;
 MEDLINE=95316841; PubMed=7796396; Fernandes:Alnemri T., Litwack G.,
 "Mch2, a family.";
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 Caspase 6 precursor (EC CASP6 OR MCH2.
 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-6 precursor (EC 3.4.22.-) (Apoptotic
 ACT_SITE
ACT_SITE
SEQUENCE
 PROCESSING
 Cancer Res.
 Homo sapiens (Human).

Metazoa; Chordata;
 P55212;
01-OCT-1996
 HUMAN
ICE6_HUMAN
 TISSUE-T-cel]
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 CHAIN
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 PROSITE; PS01122; CASPASE_CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20;
 Pfam;
Pfam;
 260
 PRINTS; PR00376; ILIBCENZYME. SMART; SM00115; CASC; 1.
 265
 200
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 PROPEP
 Hydrolase;
 InterPro;
 InterPro;
 205
 157
 80
 97
 37
 20
 Local
 Ced-3/interleukin
 FASMLTKKLHF
 IVSMLTKELYF
 SWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPC
 LFIIQACRGTELDCGIETDSGVD------
 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI
 IFIIQACRGSQHDVPVVPLDMVDHQTDKLDNVTQVDAASVYTLPAGADFLMCYSVAEGYY
 LLKIHEVSTSSHIDADCFICVFLSHGEGNHVYAYDAKIEIQTLTGLFKGDKCQSLVGKPK
 VELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKFK 156
 YKMDHKRRGVALIFNHERFFWHLTLPERRGTNADRDNLTRRFSDLGFEVKCFNDLRAEEL
 PF00655; ICE_p10; 1.
PF00656; ICE_p20; 1.
 PF00655;
 new member of the apoptotic
 Similarity
 IPR002138;
IPR001309;
 163
177
104
146
276
 Thiol
 55:2737-2742(1995).
 Conservative
 STANDARD;
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 270
 275
 Fernandes-Alnemri T.,
 protease;
 5
162
176
276
104
146
 Primates;
 L., Trapani J.A.,
 36.0%;
41.4%;
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 ICE_p20
 ICE_p10
 ₩,
 42;
 Apoptosis; Zymogen.
BY SIMILARITY.
 CASPASE-6 SUBUNIT P18 (
BY SIMILARITY,
CASPASE-6 SUBUNIT P11 (
BY SIMILARITY,
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BY SIMILARITY,
BY SIMILARITY,
 converting
 Score 526; DB 1;
Pred. No. 4.4e-37;
 Craniata; Vertebrata; Catarrhini; Hominidae
 PRT;
 Mismatches
 Alnemri E
 Ced-3/Ice
 293
 , Zangrilli J., I
 enzyme-like
 DDMACHKIPVEADFLYAYSTAPGYY
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 Hominidae;
 protease
 cysteine
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 CRC64;
 Indels
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mediator CPP32.";

J. Biol. Chem. 271:27099-27106(1996).

-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASE...

-i- FUNCTION: INVOLVED IN THE ACTIVATION. CLEAVES POLY(ADP-RIBOSE)

RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE)
 Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
 InterPro;
InterPro;
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or send an email to license@isb-sib.ch).
 EMBL; U20536; AAC50168.1;
EMBL; U20537; AAC50169.1;
HSSP; P42574; 1PAU.
MEROPS; C14.005; -.
 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no rest
 CHAIN
 Hydrolase;
PROPEP
 PROSITE;
 PROSITE;
 Genew;
 PROSITE;
 PROSITE;
 InterPro;
 MIM; 601532;
 264
 217
 204
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 157
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 97
 97
 37
 37
 SUBUNIT: HETERODIMER OF A 18 kDa (P18)
SUBCELLULAR LOCATION: CYTOPLASMIC.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPH
ARE PRODUCED BY ALTERNATIVE SPLICING.
SEEM TO HAVE PROTEOLYTIC ACTIVITY.
PTM: CLEAVAGES BY CPP32, CASPASE-8 OR
CIVSMLTKELYFY
 SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 YSWRNSKDGSWEIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIP
 LFIIQACRGTELDCGI------ETDSGVDDDMACHKIPVEADFLYAYSTAPGY
 LLKIHEVSTVSHADADCFVCVFLSHGEGNHIYAYDAKIEIQTLTGLFKGDKCHSLVGKPK
 YKMDHRRRGIALIFNHERFFWHLTLPERRRTCADRDNLTRRFSDLGFEVKCFNDLKAEEL
 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI
 YSHRETVNGSWYIQDLCEMLGKYGSSLEFTELLTLVNRKVSQRRVDFCKDPSAIGKKQVP
 IFIIQACRGNQHDVPVIPLDVVDNQTEKLDTNITEVDAASVYTLPAGADFLMCYSVAEGY
 VELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPK 156
 104;
 HGNC:1507; CASP6.
 Similarity
 PS01122; CASPASE_CYS;
PS01121; CASPASE_HIS;
PS50207; CASPASE_P10;
PS50208; CASPASE_P20;
 IPR002398; ICE.
IPR002138; ICE_p10
IPR001309; ICE_p20
 293
 Conservative
 24
180
194
121
 A.
 protease;
23
 276
 179
193
293
121
163
102
 35.4%;
 33409
 institutions as long as its content
 MW;
 42;
 Apoptosis; Zymogen; Alternative
 Score
Pred.
 is not removed. Usage by and for commerciar agreement (See http://www.isb-sib.ch/announce/
 MISSING
 CASPASE-6 SUBUNIT P11
BY SIMILARITY.
BY SIMILARITY.
 CASPASE-6 SUBUNIT P18
 BD9204E23CE1F670 CRC64;
 Mismatches
 517.5; DB 1
No. 2.4e-36;
 (IN ISOFORM BETA)
 (P18) AND A 11 kDa (P11) SUBUNIT
 ALPHA (SHOWN ING. THE BETA
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 DB 1;
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 Gaps
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CFASMLTKKLHFF

Caspase precursor (EC ICE OR CG7788.

001382; Q9VAH1; 01-NOV-1997 (Re

11-NOV-1997 (Rel. 35, 16-OCT-2001 (Rel. 40, 15-JUN-2002 (Rel. 41,

35, Created)

Last sequence upda Last annotation up 3.4.22.-) (drICE)

update)

update)

ICE\_DROME

STANDARD;

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RA Abril J.F., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Siden K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., Sheng T., Weinstock G.M., Weinscock G., Na
 -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE RESPONSIBLE FOR APOPTOSIS EXECUTION. ACTS DOWN CLEAVES BACULOVIRUS P35 AND LAMIN DMO IN VITR-
!- SUBUNIT: HETERODIMER OF A 21 kDa (P21) AND A CONTROL OF A CONTROL O
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., haril T.F., Acharati A. M. L. T. Nelson C.R., Miklos G.L.G.
 MEDLINE=20196006; PubMed=10731132;
 EMBO J. 16:2805-2813(1997).
 protease,
 Muscomorpha; Ep
NCBI_TaxID=7227
 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 SEQUENCE FROM N.A.
 Fraser A.G.,
 SEQUENCE FROM N.A.
 Identification of a Drosophila melanogaster ICE/CED-3-related
protease, drICE.";
 MEDLINE-97327558; PubMed-9184225;
 Evan G.I.;
 P35 AND LAMIN DMO IN VITRO.
OF A 21 kDa (P21) AND A 12 kDa
EXPRESSED AT ALL STAGES WHERE A
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 (P12) SUBUNIT
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C P89116;
T 01-NOV-1997 (Rel. 35, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
T 15-JUN-2002 (Rel. 41, Last annotation update)
E Caspase-1 precursor (EC 3.4.22.-)
E Caspase-1 precursor (EC 3.4.22.-)
E Spodoptera frugiperda (Fall armyworm).

S Spodoptera frugiperda (Fall armyworm).

C Eukaryota; Metazoa; Arthropoda; Mandibulata; Par
 Query Match
Best Local
 Matches
 PROPEP
CHAIN
ACT_SITE
ACT_SITE
CONFLICT
CONFLICT
 Insecta; Pterygota; Neoptera; Endopterygota;
 SEQUENCE
 CHAIN
 PROSITE; PS01122; CASPASE_CYS;
PROSITE; PS01121; CASPASE_HIS;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
 Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
 Hydrolase;
 InterPro; IPR002398;
InterPro; IPR002138;
InterPro; IPR001309;
 the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitied and this statement is not removed.
 286
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 FlyBase; FBgn0019972;
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 MEROPS; C14.015;
 EMBL; Y12261;
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 1 MENTENSVDSKSIKNLEPKII--HGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKS
 TLLTFVCQRVAVDFESCTPDTPEMHQQKQIPCITTMLTRILRF
 HILTRVNRKVATEFESFSFDA-TFHAKKQIPCIVSMLTKELYF
 T-LKSRAGTNVDCENLTRVLKQLDFEVTVYKDCRYKDILRTIEYAASQNHSDSDCILVAI
 SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 LSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGI-----E
 TGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVL
 LANGYSSPSSSYRKNVAKMVTDRHAAE----
 TETDGDSSMS
 LSHGEMGYIYAKDTQYKLDNIWSFFTANHCPSLAGKPKLFFIQACQGDRLDGGVTMQRSQ
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 P42574;
 AE003771;
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 CAA72937.1; -.
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 YKIPVHADFLIAYSTVPGFYSWRNTTRGSWFMQSLCAELAANGKRLDIL
 AAF56939.1; -.
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 DB 1;
Pancrustacea; Hexapoda
Lepidoptera; Glossata;
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 SEQUENCE
 "Spodoptera frugiperda caspase-1, a novel insect cleaves the nuclear immunophilin FKB-46, is the t baculovirus antiapoptotic protein p35.";
J. Biol. Chem. 272:1421-1424(1997).
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 InterPro; IPR002398; InterPro; IPR002138; InterPro; IPR001309;
 EMBL; U81510;
 between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no re
 Ahmad M., Srinivasula
Alnemri E.S.;
 ROPEP
 PROSITE; PS50208;
 PROSITE;
 MEROPS; C14.015;
 MEDLINE=97153084; PubMed=8999805;
 Ditrysia; Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera
 227
 170
 155
 110
 95
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 37
 Local Similarity
 PTM: AN AUTOCATALYTIC MECHANISM GENERATES TH SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 3101. Chem. 272:1421-1424(1997).
FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APPOPTOSIS EXECUTION (BY SIMILARITY). INHIBITED
THE BACULOVINUS ANTI-APOPTOTIC PROTEIN P35. CLEAVES P35 AND
 SUBUNIT: HETERODIMER
 SUBUNIT
 LTKELYF
 TRGSWFMQALCEELRYAGTERDILTLLTFVCQKVALDFESNAPDSAMMHQQKQVPCITSM
 EINKFIQQTAEMDHSDADCLLVAVLTHGELGMLYAKDTHYKPDNLWYYFTADKCPTLAGK
 YNMNHKHRGMAIIENHEHFDIH----SLKSRTGTNVDSDNLSKVLKTLGFKVTVFPNLKSE
 YKMDYPEMGLCIIINNKNF--HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTRE
 SWISS-PROT entry is copyright. It is produced through a collaboration
 PKLFIIQACRGTELDCGI----
 EIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGK 154
 KDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFD-ATFHAKKQIPCIVSM
 PKLFFIQACQGDRLDGGITLSRTETDG---SPSTSYRIPVHADFLIAFSTVPGYFSWRNT
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 PS01122; CASPASE_CYS;
PS01121; CASPASE_HIS;
PS50207; CASPASE_P10;
PS50208; CASPASE_P20;
 299
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 Conservative
293
 275
 AAC47442.1;
 1CP3.
 AA;
 protease;
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CASPASE-1 SUBUNIT I
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 ETDSGVDDDMACHKIPVEADFLYAYSTAPGYYSWRNS
 Score 470;
Pred. No. 2
 CASPASE-1 SUBUNIT P19/18
 19/18 kDa
 99F4FED09B04EEDE CRC64;
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RA Adams M.D., Celniker S.E., Holt R.A., Honders R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Bellew R.M., Basu A., Barndale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Barndale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borter J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Bordova D., Botchan M.R., Buck J., Brokstein P., Brottier P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dordova D., Botchar A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dordova D., Botchar A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibeywam C.,
RA Hill X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Kulp D., Lai Z.,
RA Kimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. H., Nelson D.L.,
RA Merkilov G., Millshina N.V., Mobarry C., Worris J., McShrefi A.,
Rount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkilov G., Millshina N.V., Mobarry C., World S., Sheeler F., Shen H.,
Rang Z.-Y., Ketchum R.S., Pollard J., Purl V., Reese M.G.,
Rang M.S., Martin
 _DROME
 MEDLINE=97153052; PubMed=8999799;
Song &., McCall K., Steller H.;
"DCP-1, a Drosophila cell death protease essential for development.";
Science 275:536-540(1997).
 002002; Q9W1NO;
15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
15-JUN-2002 (Rel. 41,
 MEDLINE=20196006; PubMed=10731132;
 STRAIN-Berkel
 SEQUENCE FROM N.A.
 Science
 Song
 Muscomorpha; Eph
NCBI_TaxID=7227;
 Caspase-1 precursor (EC DCP-1 OR CG5370.
 TISSUE-Embryo
 SEQUENCE FROM N.A.,
 Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 Eukaryota; Metazoa;
 Drosophila melanogaster (Fruit fly)
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PROSITE; PS01121; CASPASE_HIS; 1
PROSITE; PS50207; CASPASE_P10; 1
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SUBUNIT: HETERODIMER OF A 22 kDa (P22) AND A 13 kDa (P13) SUBUNIT.

DEVELOPMENTAL STAGE: PRESENT UNIFORMLY THROUGHOUT EMBRYOS OF

STAGES 4 AND 10. IN STAGE 16 EMBRYOS, THE EXPRESSION BECOMES

RESTRICTED TO THE CENTRAL NERVOUS SYSTEM, THE DEVELOPING GONADS,

AND A PORTION OF THE GUT. IN STAGE 17 EMBRYOS, EXPRESSION IS

MAINLY LOCALIZED IN CELLS ALONG THE MIDLINE OF THE CENTRAL NERVOUS
 European Bioinformatics Institute. There
 SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 DGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDAT--FHAKKQIPCIVSM:|||:|||:|||:|||:|||:|||
 PKLFFIQACQGDRLDGGITLEKGVTETDGESSTSYKIPIHADFLFSYSTIPGYFSWRNIN
 DILKHVGKAAELDHTDNDCLAVAILSHGEHGYLYAKDTQYKLDNIWHYFTATFCPSLAGK
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 NSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTRE : | | : | | : | | | : | | | : |
 LTRILRE
 LTKELYF
 NGSWYMQSLIRELNANGKKYDLLTLLTFVNQRVALDFES-NVPATPMMDRQKQIPCLTSM
 PKLFIIQACRGTELDCGIETDSGV----DDDMACHKIPVEADFLYAYSTAPGYYSWRNSK
 SEYNMSHKHRGVALIFNHE-FFDIPSLKSRTGTNVDAQELKKAFENLGFAVSVHKDCKLR
 SWISS-PROT entry is copyright. It is produced teen the Swiss Institute of Bioinformatics and
 AF001464;
AE003461;
 l Similarity
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; O14676;
 A
 AAB58237.1; -.
AAF47027.1; -.
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 protease;
 32.1%;
39.7%;
 institutions as long as its content
 Q14793;
 MW.
 46;
 2ymogen;
 Score 469; DB
Pred. No. 3.3e
46; Mismatches
 CASPASE-1 SUBUNIT BY SIMILARITY. BY SIMILARITY.
 PROBABLE
 Q14794; Q14795;
 B5FF0FF75EB8E2BD
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 Apoptosis
 DB 1,
3.3e-32;
95;
 (See http://www.isb-sib.ch/announce/
 SUBUNIT
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 Q14796; Q15780;
 Length 323;
 CRC64;
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 Gaps
 306
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SEQUENCE FROM N.A. (ISOFORM 2-ALPHA).
MEDLINE-97373543; PubMed-9228018;
Srinivasula S.M., Ahmad M., Ottilie S., Bullr
Fernandes-Alnemri T., Croce C.M., Litwack G.,
Armstrong R.C., Alnemri E.S.;
"FLAME-1, a novel FADD-1ike anti-apoptotic mo
Fas/TNFR1-induced apoptosis.";
J. Biol. Chem. 272:18542-18545(1997).
 TISSUE=T-cell;

MEDLINE=96353838; PubMed=8755496;

Rernandes-Alnemri T., Armstrong R.C., Krebs J., Srini
Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomas
Litwack G., Alnemri E.S.;

"In vitro activation of CCP32 and Mch3 by Mch4, a nov
apoptotic cysteine protease containing two FADD-like
proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 protease Mch5 is a CrmA-inhibitable protease that a Ced-3/ICE-like cysteine proteases."; Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
 Srinivasula S.M.,
Alnemri E.S.;
 PARTIAL SEQUENCE, AND PROCESSING.
MEDLINE-97121412; PubMed-8962078;
Srinivasula S.M., Ahmad M., Ferna
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDIJINE-96279827; PubMed-8681377;
Muzio M., Chinnaiyan A.M., Kischkel F.C., O'Rou
Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz
Krammer P.H., Peter M.E., Dixit V.M.;
"FLICE, a novel FADD-homologous ICE/CED-3-11ke
to the CD95 (Fas/APO-1) death-inducing signalin
 MEDLINE=97160607; PubMed=9006941;
Muzio M., Salvesen G.S., Dixit V.M.;
"FLICE induced apoptosis in a cell-free
 MEDLINE=99132295; PubMed=9931493;
Grenet J., Teitz T., Wei T., Valentine
PROCESSING
 zymogens
 Gene 226:225-232(1999).
 SEQUENCE FROM N.A.
 Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D "Involvement of MACH, a novel MORTI/FADD-interacting Fas/Apó-1- and TWE receptor-induced cell death.";
 SEQUENCE FROM N.A., AND ALTERNATI TISSUE-Thymus, and B-cell; MEDLINE-96279826; PubMed-8681376;
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-8 precursor (EC 3.4.22-) (ICE-like apoptotic protease 5)
(MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease
 8
 'Molecular ordering
 "Structure and chromosome localization
 SEQUENCE FROM N.A.
 (Apoptotic protease Mch-5) (CAP4). CASP8 OR MCH5.
 Cell 85:803-815(1996).
 Boldin M.P.,
 NCBI_TaxID=9606;
 Biol.
 85:817-827(1996).
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 272
 Ahmad M., Ottilie S., Bullrich F., T., Croce C.M., Litwack G., Tomase
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FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND THE TO THE ALAPTOR MOLECULE FADD TOWN I INDUCED CELL DEATH. BINDING TO THE ADAPTOR MOLECULE FADD RECRUITS IT TO EITHER RECEPTORS. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH PROTEDLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN LIBERATED FROM THE DISC AND FREE TO ACTIVATE DOWNSTREAM APOPTOTIC PROTEASES. PROTEDLYTIC FRAGMENTS OF THE "TERMINAL PROBEPTIDE (TERMED CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC. CLEAVES AND ACTIVATES CASPASE-3, -4, -6, -7, -9, AND -10. MAY PARTICIPATE IN THE GRANZYME BAPOPTOTIC PATHWAYS. PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMARASE (PARF). HYDROLYZES THE SMALL-MOLECULE SUBSTRATE, AC- ASP-GLU-VAL-ASP-1-AMC. LIKELY TARGET FOR THE COMPOX VIRUS CRMA DEATH INHIBITORY PROTEIN.
 EMBL;
EMBL;
EMBL;
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 IALDRACID WALF CREATA

I AALTENANTIVE PRODUCTS: 8 ISOFORMS; 1-ALPHA (SHOWN HERE), 2-ALPHA/MCH5-BETA, 3-ALPHA, 4-ALPHA, 1-BETA, 2-BETA, 3-BETA AND 4-BETA/MCH5-BETA, 3-ALPHA, 4-ALPHA, 1-BETA, 2-BETA, 3-BETA AND 4-BETA/MCH5-BETA, 3-ALPHA, 1-ALPHA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BAND/MCH5-BETA/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAND/MCH5-BAN
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EMBO J. 16:2794-2804(1997).
 Structure 7:1125-1133(1999)
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 "The three-dimensional structure of caspase-8:
 Medema J.P., Scaffidi C., Kischkel F.C., She Krammer P.H., Peter M.E.;
"FLICE is activated by association with the
 Medema
 J.C.,
 X98172; CAA66853 1; -...
X98173; CAA66854 1; -...
X98174; CAA66855 1; -...
X98175; CAA66856 1; -...
X98176; CAA66857 1; -...
X981776; CAA66857 1; -...
X981778; CAA66859 1; -...
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601763; -.
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 AF102146;
AF102139;
AF102140;
AF102141;
AF102142;
AF102143;
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AF102145;
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 U58143;
 CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 Tomaselli K.J.,
 Scaffidi
 AAC50602.1;
AAC50645.1;
 AAD24962.1; JOINED
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RESULT 15
ICE9_HUWAN STANDARD; PRT; 41:
ID ICE9_HUWAN STANDARD; PRT; 41:
AC P55211; Q92852; Q95348; Q9UIJ8; Q9UEQ3;
DT 01-OCT-1996 (Rel. 34, Created)
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Matches 1
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 InterPro; IPR001875; DED.
InterPro; IPR002138; ICE_p10.
InterPro; IPR0021309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
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 136
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 217
 77
 24
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 SESQ---
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1 216
217 374
375 384
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PS01121;
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 PS50207;
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317
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269
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199
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 Conservative
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 -TLDKVYQMKSKPRGYCLIINNHNFAKAREKVPKLHSIRDRNGTHLDAGALTT
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 CASPASE_CYS;
CASPASE_HIS;
CASPASE_P10;
CASPASE_P20;
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 DFGQSLPNEKQTSGILSDHQQSQFCKSTGESAQTSQH ISOFORM 1 BETA).
 GEELCGVMTISDSPREQDSESQTLDKVYQMKSKPRGY
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 MISSING (IN ISOFORM 3 ALPHA)
 DFGQSLPNEKQTSGILSDHQQSQFCKSTGESAQTSQH
 ALPHA AND ISOFORM 4 BETA). ERSSSLEGSPDEFSNGEELCGVMTISDSPREQDSESQ
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 CASPASE-8
 7A5FEAA6B39B582F
 Mismatches
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 (IN REF. 3 AND 5).
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(IN REF. 2 AND 4).
 (IN ISOFORM 2 BETA)
(IN ISOFORM 1 BETA)
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SEQUENCE FROM N.A.
MEDLINE=96279246; PubMed=8663294;
Grin K., Chinnaiyan A.M.,

 SEQUENCE FROM N.A.
MEDLINE-99315341; PubMed=10384055;
MEDLINE-99315341; PubMed=10384055;
Hadano S., Nasir J., Nichol K., Rasper D.M., Vaillancourt J.P.
Hadano S., Nasir J., Nichol K., Nicholson D.W., Hayden N., Hayden N.
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 the lamin-cleaving enzyme Mch2alpha
mediator CPP32.";
 Caspase 9 precursor (EC 3.4.22.-) (CASP-9) (ICE-like apoptotic protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease activating factor 3) (APAF-3).
 activity
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 Srinivasula
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 Izawa M., Mori T., Ito
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 Alnemri E.
 Armstrong
 MEDLINE=97059171; PubMed=8900201;
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
 CASP9 OR MCH6
 nhibitor
 "The Ced-3/interleukin 1beta
 "ICE-LAP6,
 Homo sapiens (Human).
 NCBI_TaxID=9606;
 16-OCT-2001 (Rel. 40, 15-JUN-2002 (Rel. 41,
 ol D.W., Billiar T.K.;

caspase-9 variant missing the catalytic site is an endogenous hibitor of apoptosis.";

Biol. Chem. 274:2072-2076(1999).

- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. BINDING OF CASPASE-9 TO PROPEOSIBLE FOR APOPTOSIS EXECUTION. BINDING OF CASPASE-9 AND 1 LEADS TO ACTIVATION OF THE PROTEASE WHICH THEN CLEAVES AND 1 LEADS TO ACTIVATION OF THE PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE)
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 the cytotoxic
 SUBUNIT: Heterodimer
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 Genome 10:757-760(1999).
 splicing "
 Chem. 271:16720-16724(1996).
 (DEC-1998) to the EMBL/GenBank/DDBJ databases
 R.C., Wang
 a novel member of the ICE/Ced-3 otoxic T cell protease granzyme
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 271:27099-27106(1996)
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ang L., Trapani J.A.,
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 Caspase-9 and APAF1 bind to each other via their respective NH2-terminal CED-3 homologous domains in the presence of cytochrome
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 PROSITE; PS50209; CARD; 1.
PROSITE; PS01122; CASPASE_CYS;
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